

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 15, 2006, 20:35:01 ; Search time 188 Seconds
(without alignments)
1836.977 Million cell updates/sec

Title: US-10-698-096-17

Perfect score: 3995
Sequence: 1 MQKNKLKLVKALPSPIDYFN.....VELSRASSRQVINFGPSIK 786

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005as:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3527	88.3	787	7	ADDD43701
2	3507.5	87.8	787	6	ABB82565
3	3507.5	87.8	787	7	ADN08758
4	3505	87.7	787	3	AAV59284
5	3505	87.7	787	8	ADG88542
6	3499.5	87.6	787	6	ABB82567
7	3243.5	81.2	788	7	ADDD43703
8	3243.5	81.2	788	7	ADN08783
9	3239	81.0	788	7	ADN08753
10	3235	81.0	788	7	ADN08762
11	3182.5	79.7	789	2	AAW46862
12	3182.5	79.7	789	2	AAW46862
13	3180.5	79.6	789	2	AAW46863
14	3180.5	79.6	789	2	AAW46863
15	3176.5	79.5	789	2	AAW46867
16	3176.5	79.5	789	2	AAW46867
17	3175.5	79.5	789	2	AAW46867
18	3175.5	79.5	789	2	AAW46867
19	3175.5	79.5	789	2	AAW46867
20	3175.5	79.5	789	2	AAW46867
21	3175.5	79.5	789	2	AAW46867
22	3171.5	79.4	789	2	AAW46867
23	3171.5	79.4	789	2	AAW46867
24	3171.5	79.4	789	2	AAW46867

25	3171.5	79.4	789	8	ADN61600	ADN61600 VIP3A tox
26	3171.5	79.4	789	9	AEA62843	AEA62843 Bacillus
27	3171.5	79.4	789	9	AEA61740	AEA61740 Bacillus
28	3171.5	79.4	809	2	AAW19521	AAW19521 VIP3A(a)
29	3171.5	79.4	809	2	AAW19521	AAW19521 B. cereus
30	3171.5	79.4	809	2	AAW46732	AAW46732 Maize Opt
31	3170.5	79.4	789	2	AAW46860	AAW46860 Bacillus
32	3170.5	79.4	789	2	AAW46868	AAW46868 Bacillus
33	3170.5	79.4	789	2	AAW46869	AAW46869 Bacillus
34	3170.5	79.4	789	2	AAW46871	AAW46871 Bacillus
35	3170.5	79.4	789	2	AAW46872	AAW46872 Bacillus
36	3170.5	79.4	789	2	AAW46873	AAW46873 Bacillus
37	3167.5	79.3	789	2	AAW80320	AAW80320 Bacillus
38	3167.5	79.3	789	2	AAW80320	AAW80320 Bacillus
39	3160	79.1	786	7	ADDD43705	ADDD43705 Bacillus
40	3158.5	79.1	790	2	AAW60215	AAW60215 Bacillus
41	3156.5	79.0	789	2	AAW91244	AAW91244 B. thurin
42	3156.5	79.0	789	2	AAW19515	AAW19515 B. cereus
43	3156.5	79.0	789	2	AAW80321	AAW80321 Bacillus
44	3156.5	79.0	789	2	AAW46726	AAW46726 Native ve
45	3151	78.9	790	2	AAW46872	AAW46872 Bacillus

ALIGNMENTS

RESULT 1
ADD43701
ID ADD43701 standard; protein; 787 AA.
XX
AC ADD43701;
XX
DT 15-JAN-2004 (first entry)
XX
DE Bacillus thuringiensis insecticidal protein ISP3-1099E.
XX
KW Insecticidal; plant insect pest; pesticide.
XX
OS Bacillus thuringiensis.
XX
PN W02003080656-A1.
XX
PD 02-OCT-2003.
XX
PF 20-MAR-2003; 2003MO-EP003068.
XX
PR 22-MAR-2002; 2002US-0366276P.
XX
PR 06-NOV-2002; 2002US-0423999P.
XX
PA (PARB) BAYER BIOSCIENCE NV.
XX
PI Arnaut G, Boets A, De Rudder K, Vanneste S, Van Rie J;
XX
XX WPI; 2003-876903/81.
XX
DR N-PSDB; ADD43700.
XX
PT New insecticidal proteins, useful for controlling plant insect pests, and
PT for increasing resistance to insect damage compared to control plants.
XX
XX Claim 3; SEQ ID NO 2; 81pp; English.
XX
XX The present invention relates to Bacillus thuringiensis insecticidal
XX proteins (ADD43701, ADD43703 and ADD43705) and their coding sequences
XX (ADD43700, ADD43702 and ADD43704). The insecticidal proteins are
XX insecticidal against Helicoverpa zea, Heliothis virescens, Ostrinia
XX nubilalis, Spodoptera frugiperda, Agrotis ipsilon, Pectinophora
XX gossypiella, Scirphophaga incertulas, and Anticarsia gemmatilis. Sesamia
XX inferens, Chilo partellus and Anticarsia gemmatilis. The proteins are
XX useful for controlling plant insect pests, and for increasing resistance
XX to insect damage compared to control plants.
XX
XX Sequence 787 AA;

Query Match 88.3%; Score 3527; DB 7; Length 787;
 Best Local Similarity 87.5%; Pred. No. 3,7e-208;
 Matches 685; Conservative 43; Mismatches 55; Indels 0; Gaps 0;

4 NNLKSLVALPSFIDYFNGIYGAFGKIDIMMIFKMTGSDLTDELTKNOQLNEISGK 63
 5 NTKLNARALPSFIDYFNGIYGAFGKIDIMMIFKMTGSDLTDELTKNOQLNEISGK 64
 64 LDGVNGLNDLLAOGNLDTELSEKELIKIANEQNVLDVNTKLDANIMLNTYLPKITS 123
 65 LDGVNGLNDLLAOGNLDTELSEKELIKIANEQNVLDVNTKLDANIMLNTYLPKITS 124
 124 LSDVMKQNYALGLQIEIYSKQLEISDKLDIVNVNVLINSTLTETTPAYORIKYVNEKE 183
 125 LSDVMKQNYALSLQIEIYSKQLEISDKLDIVNVNVLINSTLTETTPAYORIKYVNEKE 184
 184 ALTSATETNLKTQDSSHTDILDELTELTAASVTKNVDGFEFYNTFHDVWGNLNF 243
 185 ELTFATETTLTKVEDSSPADILDELTELTAASVTKNVDGFEFYNTFHDVWGNLNF 244
 244 GRGALKTASELIAKENIKTSGSEVGNVNFILVLTALQAKAFLLTTCRKLLGLADIDYT 303
 245 GRGALKTASELIAKENIKTSGSEVGNVNFILVLTALQAKAFLLTTCRKLLGLADIDYT 304
 304 PINNEHLNKEKEEPRVNIPLTSLNTSPNTEKARSGDKAKIIMEAKPGYALVGEISK 363
 305 SINNEHLNKEKEEPRVNIPLTSLNTSPNTEKARSGDKAKIIMEAKPGYALVGEISM 364
 364 DSIALVKVYQAKLKHNYQIDKDSLSEIYGDIDKLLCPDSEOMYVYNNKIAFPNEVYITK 423
 365 DSMTVLKAYQAKLKQDYQVDKDSLSEIYGDIMNKLCPDSEOMYVYNNKIAFPNEVYITK 424
 424 IATFKLNSLRVEVTANFYDSTGDIIDLNKKLIESSEAFPSMLNANNGVYMEIGTISSET 483
 425 LFTFKKNSLRVEVTANFYDSTGDIIDLNKKLIESSEAFPSMLNANNGVYMEIGTISSET 484
 484 FLTPINGFGIYDENSRLVLTCKSYLRETLATDLSNKEKLIIVPENGFSINIVENG 543
 485 FLTPINGFGIYDENSRLVLTCKSYLRETLATDLSNKEKLIIVPENGFSINIVENG 544
 544 EGENLEPMKANNKAAVVDHTGAVNGTKVLVHEDGEPSPGIDKLKLTETVVOYIVK 603
 545 EGENLEPMKANNKAAVVDHTGAVNGTKVLVHEDGEPSPGIDKLKLTETVVOYIVK 604
 604 AAIYLDKEXGDIYIEETNNLEDFQAVTKRFTGTDSRVHLIFTSONGEBAFGANFII 663
 605 AAIYLDKEXGDIYIEETNNLEDFQAVTKRFTGTDSRVHLIFTSONGEBAFGANFII 664
 664 SEIRPSEELISPELLISDAWVGSGTWISGNSLANSVNGTRQNLISLSTYSMTN 723
 665 SEIRPSEELISPELLISDAWVGSGTWISGNSLANSVNGTRQNLISLSTYSMTN 724
 724 VNGFGVITIRNSREVEFERSYLOPSSKYISEKFTTTNTTGLVLEISPRASRGVIFGDP 783
 725 IINGFGVITIRNSREVEFERSYLOPSSKYISEKFTTTNTTGLVLEISPRASRGVIFGDP 784
 784 SIK 786
 785 SIK 787

RESULT 2
 ABB82565
 ID ABB82565 standard; protein; 787 AA.
 AC ABB82565;
 XX
 DT 04-FEB-2003 (first entry)
 XX
 DE B. thuringiensis native Vip3B polypeptide.
 XX
 KW Vip3; toxin; insecticide; transgenic; delta-endotoxin; Vip3B.
 XX

OS Bacillus thuringiensis.
 XX
 PN WO200278437-A2.
 XX
 PD 10-OCT-2002.
 XX
 PF 01-APR-2002; 2002WO-US010264.
 XX
 PR 30-MAR-2001; 2001US-0280025P.
 XX 04-DEC-2001; 2001US-0336657P.
 XX
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX
 PI Miles P, Kramer V, Shen Z, Shotkoski F, Warren GW;
 XX
 DR WPI: 2003-040603/03.
 DR N-PSDB; ABV74977.
 PT Novel pesticidal toxin, designated Vip3 toxins from Bacillus
 PT thuringiensis, useful for controlling insects, e.g., lepidopteran insect,
 PT is highly active against a wide range of insect pests.
 XX
 PS Claim 4; Page 56-60; 82pp; English.
 XX
 CC The invention relates to an isolated Vip3 toxin from B. thuringiensis
 CC that is active against insects. The toxins are useful for controlling
 CC insects, where the insect is a lepidopteran insect selected from Ostrinia
 CC nubilalis (European corn borer), Plutella xylostella (diamondback moth),
 CC Spodoptera frugiperda (fall armyworm), Agrotis ipsilon (black cutworm),
 CC Helioverpa zea (corn earworm), Helioverpa punctigera (tobacco budworm),
 CC Helioverpa armigera (cotton bollworm), Manduca sexta (tobacco hornworm),
 CC Trichoplusia ni (cabbage looper), Pectinophora gossypiella (pink
 CC bollworm), and Cochylis hospes (banded sunflower moth). The
 CC polynucleotides encoding the toxins are useful to produce an insect-
 CC resistant transgenic plant. The toxins are useful in combination with Bt
 CC delta-endotoxins to increase pest target range. The present sequence
 CC represents a B. thuringiensis Vip3 toxin
 XX

Sequence 787 AA;
 SQ

Query Match 87.8%; Score 3507.5; DB 6; Length 787;
 Best Local Similarity 87.3%; Pred. No. 5.9e-207;
 Matches 687; Conservative 46; Mismatches 53; Indels 1; Gaps 1;

1 MOKNN-KLSVKKLPSFIDYFNGIYGAFGKIDIMMIFKMTGSDLTDELTKNOQLNE 59
 1 MOKNNKLNARALPSFIDYFNGIYGAFGKIDIMMIFKMTGSDLTDELTKNOQLNE 60
 60 ISGKLDGVNGLNDLLAOGNLDTELSEKELIKIANEQNVLDVNTKLDANIMLNTYLPK 119
 61 ISGKLDGVNGLNDLLAOGNLDTELSEKELIKIANEQNVLDVNTKLDANIMLNTYLPK 120
 120 ITSMISDVKKQNYALGLQIEIYSKQLEISDKLDIVNVNVLINSTLTETTPAYORIKYV 179
 121 ITSMISDVKKQNYALSLQIEIYSKQLEISDKLDIVNVNVLINSTLTETTPAYORIKYV 180
 180 EKFEALTSATETNLKTQDSSHTDILDELTELTAASVTKNVDGFEFYNTFHDVWGNL 239
 181 EKFEALTSATETNLKTQDSSHTDILDELTELTAASVTKNVDGFEFYNTFHDVWGNL 240
 240 NNLPGRSALKTASELIAKENIKTSGSEVGNVNFILVLTALQAKAFLLTTCRKLLGLAD 299
 241 NNLPGRSALKTASELIAKENIKTSGSEVGNVNFILVLTALQAKAFLLTTCRKLLGLAD 300
 300 IYTPINMEHLNKEKEEPRVNIPLTSLNTSPNTEKARSGDKAKIIMEAKPGYALVGF 359
 301 IYTPINMEHLNKEKEEPRVNIPLTSLNTSPNTEKARSGDKAKIIMEAKPGYALVGF 360
 360 EISKQSIIVLVKAYQAKLKHNYQIDKDSLSEIYGDIDKLLCPDSEOMYVYNNKIAFPNE 419
 361 EISKQSIIVLVKAYQAKLKQDYQVDKDSLSEIYGDIMNKLCPDSEOMYVYNNKIAFPNE 420

QY 420 VITKIAFTKQLNSLRVEVTANFYDSSTGDIIDLNKKKLESSEAEFSMLNANDGYMPIGT 479
DB 421 VITKITFTKKGNLSRVEATANFYDSSITGDIIDLNKTKVSSSEAEVSTLSASTDGYMPLGI 480
QY 480 ISEFFLPINGFGLVDENSLVLTCKSYLRETLATDLSNKETKLIIPPNGFISNIVE 539
DB 481 ISEFFLPINGFGLVDENSLVLTCKSYLRETLATDLSNKETKLIIPPNGFISNIVE 540
QY 540 NGNLEGENLEBPWKANNKAAVYDHTGVNGTKVLYVHEDGESOPFGDKLKTEYVIOYI 599
DB 541 NGNLEGENLEBPWKANNKAAVYDHTGVNGTKVLYVHEDGESOPFGDKLKTEYVIOYI 600
QY 600 VKGKAAIYLLKDEKNGDYIYEETNNLEBDPOAVTKRFTITGDSRVHLIFTSONGEBAFG 659
DB 601 VKGKASILLKDEKNGDCIYEDTNNLEBDPQTITKSFITGDSGCVHLIFNSQNGDEAFGE 660
QY 660 NFIISIRPSEELLSPELIKSDAMVSGQTWISGNSLINSNVNGTFRQNLSESYSTYS 719
DB 661 NFIISIRLSEDLSPELINSDAWVSGQTWISGNSLINSNVNGTFRQNLSESYSTYS 720
QY 720 MNFVNGFGKVTIRNSREVVPERSYLOPSSKTISEKFTTTNNGLYVELSRASRGVIN 779
DB 721 MNFVNGFGKVTIRNSREVLPEKNYPOLSPDISKFTTAAANNGLYVELSRFTSGGAIN 780
QY 780 FGDFSIX 786
DB 781 FRNFSIK 787

RESULT 3
ADN08758
ID ADN08758 standard; protein; 787 AA.
XX

AC ADN08758;

DT 17-JUN-2004 (first entry)

DE B. churingiensis vip3B protein SEQ ID NO:7.

XX vip3C; toxin; protease inhibitor; lepidopteron; tobacco budworm;
KM sunflower head moth; beet armyworm; insect-resistance; maize; vip3B.

XX Bacillus churingiensis.

OS WO2003075655-A2.

PN 18-SEP-2003.

PD 20-FEB-2003; 2003WO-US004735.

PF 06-MAR-2002; 2002US-0362250P.

PR (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Shen Z, Warren GW, Shokoski F, Kramer V;

PI WPI: 2003-788166/74.

DR N-PSDB; ADN08757.

XX New Vip3 toxin encoded by a nucleic acid from *Bacillus churingiensis*,
PT useful for controlling lepidopteron insects such as tobacco budworm,
PT sunflower head moth or beet armyworm, or for producing an insect-
PT resistant transgenic plant.

PS Example 10; SEQ ID NO 7; 118bp; English.

CC The invention relates to a novel isolated Vip3 toxin that is active
CC against insects. The toxin acts as a protease inhibitor. The Vip3 toxin,
CC hybrid toxin and nucleic acid molecules are useful for controlling
CC lepidopteron insects such as tobacco budworm, sunflower head moth or beet
CC armyworm, for producing an insect-resistant transgenic plant, and
CC protecting a maize plant against at least one insect pest. The present
CC sequence represents native B. churingiensis vip3B.

XX
SQ Sequence 787 AA;

Query Match 87.8%; Score 3507.5; DB 7; Length 787;
Beet Local Similarity 87.3%; Pred. No. 5.9e-207;
Matches 687; Conservative 46; Mismatches 53; Indels 1; Gaps 1;

QY 1 MQKN-KLSVYKALSPFIDYFNGIYGPATGIDINMMI-FKNTYGGDLTDEILKNOQLNE 59
DB 1 MKNKNTKLNARALSPFIDYFNGIYGPATGIDINMMI-FKIDTGGNLTLDEILKNOQLNE 60
QY 60 ISGLDGVNGLNDLLAQNLDTLSEKILKIANEONKVLNDVNTKLDALIMLNTYLPK 119
DB 61 ISGLDGVNGLNDLLAQNLDTLSEKILKIANEONKVLNDVNTKLDALIMLNTYLPK 120
QY 120 ITSMLDVMKONVYALGQIEYLSKQLKISPKLDVINNVNLINSTLEITPAYORIKYVN 179
DB 121 ITSMLDVMKONVYALGQIEYLSKQLKISPKLDVINNVNLINSTLEITPAYORIKYVN 180
QY 180 EKFEALTSATETNLKTKODSSHMDILDELTELAKSVTKNDVDGPEFYNTFHDWVG 239
DB 181 EKFEALTSATETNLKTKODSSHMDILDELTELAKSVTKNDVDGPEFYNTFHDWVG 240
QY 240 NNLFGRSALKTASSELIAKENLKTSGSEVGVNVEFLIYLTALQAKAFLLTTCRKLGLAD 299
DB 241 NNLFGRSALKTASSELIAKENVKTSGSEVGVNVEFLIYLTALQAKAFLLTTCRKLGLAD 300
QY 300 IDYTPINNEHLNKEKEFRVNIILPTLSNTSPNPEYKARSDKDAKIIMEAKPGYALVF 359
DB 301 IDYTPINNEHLNKEKEFRVNIILPTLSNTSPNPEYKARSDKDAKIIMEAKPGYALVF 360
QY 360 EISKDSIAYLKVYQAKLKNVQIDKDSLSEIVYGDIDKLCPPDSEOMYYNTKIAFPREY 419
DB 361 EISKDSIAYLKVYQAKLKNVQIDKDSLSEIVYGDIDKLCPPDSEOMYYNTKIAFPREY 420
QY 420 VITKIAFTKQLNSLRVEVTANFYDSSTGDIIDLNKKKLESSEAEFSMLNANDGYMPIGT 479
DB 421 VITKITFTKKGNLSRVEATANFYDSSITGDIIDLNKTKVSSSEAEVSTLSASTDGYMPLGI 480
QY 480 ISEFFLPINGFGLVDENSLVLTCKSYLRETLATDLSNKETKLIIPPNGFISNIVE 539
DB 481 ISEFFLPINGFGLVDENSLVLTCKSYLRETLATDLSNKETKLIIPPNGFISNIVE 540
QY 540 NGNLEGENLEBPWKANNKAAVYDHTGVNGTKVLYVHEDGESOPFGDKLKTEYVIOYI 599
DB 541 NGNLEGENLEBPWKANNKAAVYDHTGVNGTKVLYVHEDGESOPFGDKLKTEYVIOYI 600
QY 600 VKGKAAIYLLKDEKNGDYIYEETNNLEBDPOAVTKRFTITGDSRVHLIFTSONGEBAFG 659
DB 601 VKGKASILLKDEKNGDCIYEDTNNLEBDPQTITKSFITGDSGCVHLIFNSQNGDEAFGE 660
QY 660 NFIISIRPSEELLSPELIKSDAMVSGQTWISGNSLINSNVNGTFRQNLSESYSTYS 719
DB 661 NFIISIRLSEDLSPELINSDAWVSGQTWISGNSLINSNVNGTFRQNLSESYSTYS 720
QY 720 MNFVNGFGKVTIRNSREVVPERSYLOPSSKTISEKFTTTNNGLYVELSRASRGVIN 779
DB 721 MNFVNGFGKVTIRNSREVLPEKNYPOLSPDISKFTTAAANNGLYVELSRFTSGGAIN 780
QY 780 FGDFSIX 786
DB 781 FRNFSIK 787

RESULT 4
AAV59284

ID AAV59284 standard; protein; 787 AA.

AC AAV59284;

DT 18-APR-2000 (first entry)

DE SUP toxin from B. churingiensis strain KB59A4-6.

XX Bacillus thuringiensis; toxin; endotoxin; pesticide; plant pest;
 KW lepidopterans; cleopterans.
 XX
 XX Bacillus thuringiensis.
 OS
 PN W09957282-A2.
 XX
 PD 11-NOV-1999.
 XX
 PF 06-MAY-1999; 99WC-US009997.
 XX
 PR 06-MAY-1998; 98US-00073898.
 PA
 XX (MYCO) MYCOGEN CORP.
 XX
 PI Feltelson JS, Schnepf HE, Narva KE, Stockhoff BA, Schmeits J;
 PI Loewer D, Dullum CJ, Muller-Cohn J, Stamp L, Morrill G;
 PI Finstad-Lee S;
 DR WPI; 2000-096811/08.
 DR N-PSDB; AAZ58823.
 XX
 PT New polynucleotides encoding pesticidally active proteins, useful for
 PT transforming plants for controlling pests.
 PS
 XX Claim 2; Page 100-103; 104pp; English.
 XX
 CC The invention relates to novel B. thuringiensis isolates, and genes
 CC encoding pesticidal toxins which are toxic to non-mammalian pests. The
 CC genes are useful in the control of non-mammalian pests and especially
 CC plant pests (e.g. lepidopterans and/or coleopterans). The polynucleotides
 CC are useful for transforming plants for controlling plant pests; for
 CC designing primers and probes useful for the identification and
 CC characterization of genes which encode pesticidal toxins. The present
 CC sequence represents a B.t. SUP toxin
 CC
 SQ Sequence 787 AA;
 Query Match 87.7%; Score 3505; DB 3; Length 787;
 Best Local Similarity 87.1%; Pred. No. 8.4e-207;
 Matches 682; Conservative 45; Mismatches 56; Indels 0; Gaps 0;

DB 425 IDFTKKAKRLRYEVTANSYDSTGEIDLANKKVVSEAEYRTL SANNDGVYMPGIVSET 484
 QY 484 FLTPINGFGVVDENSLVTLTCKSYRETLATDLSNKKETKILVPPNGFISNVENGSL 543
 DB 485 FLTPINGFGVVDENSLVTLTCKSYRETLATDLSNKKETKILVPPISFISNVENGSL 544
 QY 544 EGENLEBPWKANNKQAVYDHTGVNGTKLVYHEDGFEFQFIDKLKLTQEVYIYKAGK 603
 DB 545 EGENLEBPWKANNKQAVYDHTGVNGTKLVYHEDGFEFQFIDKLKLTQEVYIYKAGK 604
 QY 604 AAIYLDKQKQDYIYEETNLEDFQAVYKRFITGTDSSVHLIFTSQNGEAFAGNFII 663
 DB 605 ASIYLDKQKQENSIYEETNLEDFQAVYKRFITGTDSSVHLIFTSQNGEAFAGNFII 664
 QY 664 SEIRPSEELISPELISDAWVGSGQTMISGNSLINSNVNCTFRONLSLESTYSNVEN 723
 DB 665 SEIRTSSEELISPELISDAWVGSGQTMISGNSLINSNVNCTFRONLSLESTYSNVEN 724
 QY 724 VNGFGKVTIINSREVVFERSYLQFSSKYISEKFTTTNNGLVYELSRASSRGVYNGDF 783
 DB 725 VNGFGKVTIANSREVVFERSYLQFSSKYISEKFTTTNNGLVYELSRASSRGVYNGDF 784
 QY 784 SIX 786
 DB 785 SIX 787
 RESULT 5
 ADG88542
 ID ADG88542 standard; protein; 787 AA.
 XX
 AC ADG88542;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE Bacillus thuringiensis strain KB59A4-6 SUP toxin protein.
 XX
 KM Pesticide; genetic engineering; resistance; toxin; insecticide;
 KM plant protectant; gene; ds.
 XX
 OS Bacillus thuringiensis.
 XX
 PN US6603063-B1.
 XX
 PD 05-AUG-2003.
 XX
 PF 07-MAY-1999; 99US-00307106.
 XX
 PR 07-MAY-1999; 99US-00307106.
 XX
 PA (MYCO) MYCOGEN CORP.
 XX
 PI Feltelson JS, Schnepf HE, Narva KE, Stockhoff BA, Schmeits J;
 PI Loewer D, Dullum CJ, Muller-Cohn J, Stamp L, Morrill G;
 PI Finstad-Lee S;
 DR WPI; 2004-008371/01.
 DR N-PSDB; ADG88541.
 XX
 PT New polynucleotide from Bacillus subtilis, which encodes delta endotoxins
 PT or pesticide proteins, useful in plant genetic engineering, particularly
 PT for producing plants that are resistant to lepidopteran or coleopteran
 pests.
 PS
 XX Claim 1; SEQ ID NO 54; 51pp; English.
 XX
 CC The present invention provides an isolated polynucleotide from Bacillus
 CC thuringiensis (B.t.) strain KB59A4-6 that encodes an active pesticidal
 CC SUP toxin protein. The invention is useful in plant genetic engineering
 CC particularly producing plants that express such gene in order to
 CC effectively control various insects e.g. boll weevil, black cutworm etc.
 CC The invention is also useful for conferring resistance in plants against
 CC lepidopterans or coleopterans. The present sequence is Bacillus

QY 360 EISKDSIAVLKQYQAKLKHNYQIDKDSLSEIYVGDIDKLLCPDQSEQMYTNNKIAFENEY 419
DB 361 EISNDSTVLKVEAKLKQNYQVDKDSLSEIYVGDMDKLLCPDQSEQIYTTNNIVFENEY 420
QY 420 VITKIAFTKTLNSRYEVTANFVDSSGTDIDLNKKIESSEAESEFMTLANNDDGYMPLG 479
DB 421 VITKIDFTKTKLRYEVTANFVDSSGTDIDLNKKYESSAEERYTLISANDDGYMPLG 480
QY 480 ISETFLTPINGFGLVVDENSRVLVTLTCKSYLRETLATDLSNKKETKLIVPNGFISNIYE 539
DB 481 ISEFPLTPINGFGLQADENSRLLITLTKCYLRELLATDLSNKKETKLIVPNGFISNIYE 540
QY 540 NGULEGENLEPFWKANNKNAVVDHTGVNGTKVLVYHEDGESQFIDGKLKLTBYVQYI 599
DB 541 NGSEIBEDNLEPFWKANNKNAVVDHTGVNGTKVLVYHEDGESQFIDGKLKLTBYVQYI 600
QY 600 VKKKAATYLDKKNQDVIYEETNNLEDFQAVTKRFTITGDDSRVHLIFPSQNGEAFPG 659
DB 601 VKGKASTLKDKNQDCIYEDTNNGLDFQITKSFITGDDSGVHLIFPSQNGEAFPG 660
QY 660 NFIISEIRPEEELSPELIKSDAMVGSQGTWISGNSLINSNVNGTFRQMLSESYSTYS 719
DB 661 NFIISEIRSEDLSPELINSAMVGSQGTWISGNSLINSNVNGTFRQMLSESYSTYS 720
QY 720 MNTNVNGFKVYTRNSREVVPERSYIQFSSKYISEKFTTTNTGLVVELSRASSRVIN 779
DB 721 MNTNVNGFAKVTYRNSREVLFEKNYPQLSPKDISSEKFTTANNTGLVVELSRFGAIN 780
QY 780 FGDPSTK 786
DB 781 FRNPSIK 787

RESULT 7
ID ADD43703 standard; protein; 788 AA.
AC ADD43703;
XX
DT 15-JAN-2004 (first entry)
XX
DE Bacillus thuringiensis insecticidal protein ISP3-327D.
XX
KW Insecticidal; plant insect pest; pesticide.
OS Bacillus thuringiensis.
XX
PN MO2003080656-A1.
XX
PD 02-OCT-2003.
XX
PF 20-MAR-2003; 2003MO-BP003068.
XX
PR 22-MAR-2002; 2002US-0366276P.
XX
PR 06-NOV-2002; 2002US-0423999P.
XX
PA (FARB) BAYER BIOSCIENCE NV.
PI Arnaud G, Boets A, De Rudder K, Vanneste S, Van Rie J;
XX
DR MPI; 2003-876903/81.
DR N-PSDB; ADD43702.
XX
PT New insecticidal proteins, useful for controlling plant insect pests, and
XX
XX for increasing resistance to insect damage compared to control plants.
PS Claim 1; SEQ ID NO 4; 81pp; English.
XX
CC The present invention relates to Bacillus thuringiensis insecticidal
CC proteins (ADD43701, ADD43703 and ADD43705) and their coding sequences
CC (ADD43700, ADD43702 and ADD43704). The insecticidal proteins are
CC insecticidal against Helicoverpa zea, Heliothis virescens, Ostrinia
CC nubilalis, Spodoptera frugiperda, Agrotis ipsilon, Pectinophora

CC goseypjella, Scirphophaga incertulans, Cnaphalocrocis medinalis, Sesamia
CC inferens, Chilo partellus and Anticarsia gemmatilis. The proteins are
CC useful for controlling plant insect pests, and for increasing resistance
CC to insect damage compared to control plants.
XX
SQ Sequence 788 AA;
Query Match 81.2%; Score 3243.5; DB 7; Length 788;
Best Local Similarity 80.9%; Pred. No. 1e-190;
Matches 634; Conservative 65; Mismatches 84; Indels 1; Gaps 1;
QY 4 NNTLSVVALPSFIDYNGIYGFATGIDKIDNMIFKNTNGGDLTLDELKXQQLNEISGK 63
DB 5 NTKLNAAPLPSFYDFNGIYGFATGIDKIDNMIFKNTNGGDLTLDELKXQQLNEISGK 64
QY 64 LDGVNGLNDILAQNLDELTELSEIKLIEQKQVLDVNTKLDANIMNTLPTKITS 123
DB 65 LDGVNGLNDILAQNLDELTELSEIKLIEQKQVLDVNTKLDANIMNTLPTKITS 124
QY 124 LSDVMKQNYALGHQIEYLSKQLEISDKLDVINVNLINSTLRETPAYORIKYVNEKPE 183
DB 125 LSDVMKQNYALSLQIEYLSKQLEISDKLDVINVNLINSTLRETPAYORIKYVNEKPE 184
QY 184 ALTSATETMLTKYQDSSHTDIDELTELAKSVTRKNDVGEFYLANTFHVMIGNNLF 243
DB 185 ELTFATETMLTKYQDSSHTDIDELTELAKSVTRKNDVGEFYLANTFHVMIGNNLF 244
QY 244 GRSALTKASBLAKENLKTSGSEVGNVNFVLVTLQAKPLTLTCKRLGLADIDYT 303
DB 245 GRSALTKASBLAKENLKTSGSEVGNVNFVLVTLQAKPLTLTCKRLGLADIDYT 304
QY 304 PINNEHLNKEKEEFRRVNIPLTSLNTPSNPYEKARGSDAKLIMEAKGYALVGEISK 363
DB 305 SINNEHLNKEKEEFRRVNIPLTSLNTPSNPYEKARGSDAKLIMEAKGYALVGEISK 364
QY 364 DSIYAVLKVYQAKLKHNYQIDKDSLSEIYVGDIDKLLCPDQSEQMYTNNKIAFENEYITK 423
DB 365 DSIYAVLKVYEAQKLKHNYQVDKDSLSEIYVGDIDKLLCPDQSEQIYTTNNIVFENEYITK 424
QY 424 IAFTKTLNSRYEVTANFVDSSGTDIDLNKKIESSEAEFMTLANNDDGYMPLG 483
DB 425 IAFTKTLNSRYEVTANFVDSSGTDIDLNKKYESSAEERYTLISANDDGYMPLG 484
QY 484 FLTPINGFGLVVDENSRVLVTLTCKSYLRETLATDLSNKKETKLIVPNGFISNIYVNGNL 543
DB 485 FLTPINGFGLQADENSRLLITLTKCYLRELLATDLSNKKETKLIVPNGFISNIYVNGNL 544
QY 544 EGENLEPFWKANNKNAVVDHTGVNGTKVLVYHEDGESQFIDGKLKLTBYVQYIYVKGK 603
DB 545 EGENLEPFWKANNKNAVVDHTGVNGTKVLVYHEDGESQFIDGKLKLTBYVQYIYVKGK 604
QY 604 AATYLDKKNQDVIYEETNNLEDFQAVTKRFTITGDDSRVHLIFPSQNGEAFPGNFII 663
DB 605 PSIHLDKENTGYIHYDITNNNLKDVQITTKRFTITGDLGVYLLKQNGDEAMGKFTI 664
QY 664 SEIRPEEELSPELIKSDAMVGSQGTWISGNSLINSNVNGTFRQMLSESYSTYSMNFR 723
DB 665 LEIKPAEDLSPELIPNSWITTPGASISGNLFINLGNNGTFRQMLSESYSTYSISFT 724
QY 724 VNGFGVYTRNSREVVPERSYIQFSSKYISEKFTTTNTGLVVELSRAS-SRGVINFGD 782
DB 725 ASGPFVNTYRNSREVLFEKNSLMSYSTHISGFTESNNTGLVVELSRSGGGHISFEN 784
QY 783 FSIX 786
DB 785 VSIX 788

RESULT 8
ADN08783
ID ADN08783 standard; protein; 788 AA.
AC ADN08783;

```

XX 17-JUN-2004 (first entry)
DT
XX B. thuringiensis vip3C-12168 protein SEQ ID NO:32.
DE
XX vip3c; toxin; protease inhibitor; lepidopteran; tobacco budworm;
KM sunflower head moth; beet armyworm; insect-resistance; maize.
XX
OS Bacillus thuringiensis.
XX
PN WO2003075655-A2.
XX
PD 18-SEP-2003.
XX
PF 20-FEB-2003; 2003WO-US004735.
XX
PR 06-MAR-2002; 2002US-0362250P.
XX
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
PI Shen Z, Warren GW, Shothoski F, Kramer V;
XX
DR WPI; 2003-788166/74.
DR N-PSDB; ADN08782.
XX
XX New Vip3 toxin encoded by a nucleic acid from Bacillus thuringiensis,
PT useful for controlling lepidopteran insects such as tobacco budworm,
PT sunflower head moth or beet armyworm, or for producing an insect-
PT resistant transgenic plant.
XX
PS Claim 12; SEQ ID NO 32; 118bp; English.
XX
CC The invention relates to a novel isolated Vip3 toxin that is active
CC against insects. The toxin acts as a protease inhibitor. The Vip3 toxin,
CC hybrid toxin and nucleic acid molecules are useful for controlling
CC lepidopteran insects such as tobacco budworm, sunflower head moth or beet
CC armyworm, for producing an insect-resistant transgenic plant, and
CC protecting a maize plant against at least one insect pest. The present
CC sequence represents vip3c protein vip3C-12168.
XX
SQ Sequence 788 AA;
81.2%; Score 3243.5; DB 7; Length 788;
Query Match Best Local Similarity 80.9%; Pred. No. 1e-190;
Matches 634; Conservative 65; Mismatches 84; Indels 1; Gaps 1;
QY 4 NNKLSVRLPSFIDYFNGIYGFATGIDIMNMIFKTTNTGDLTLDLILKNOQLINBISGK 63
DB 5 NTKLNARALPSFIDYFNGIYGFATGIDIMNMIFKTTNTGDLTLDLILKNOQLINBISGK 64
QY 64 LDGVNGSLNDLAAQNDLTLSKELIKANQONKVDVNTKLDALINMLNTTYLPKITSM 123
DB 65 LDGVNGSLNDLAAQNDLTLSKELIKANQONKVDVNTKLDALINMLNTTYLPKITSM 124
QY 124 LSDVMKONVALGLQIEYLSKQLKEISDKLDVINNVNLNSTLTETTPAYORIKVYNEKEE 183
DB 125 LSDVMKONVALGLQIEYLSKQLKEISDKLDVINNVNLNSTLTETTPAYORIKVYNEKEE 184
QY 184 ALTSATETNLTCKODSSHDTLDELTELTELAKSVTKNDVDFEFLYNTFFDVMIGNLFF 243
DB 185 ELTFPATETTLTKVKKODSPADILDELTELTELAKSVTKNDVDFEFLYNTFFDVMIGNLFF 244
QY 244 GRSALKTRASELIAENLKTSSSEYGNVYVPLIYVTAQAQKFLTLTTCRKLGLADIDYT 303
DB 245 GRSALKTRASELIAENLKTSSSEYGNVYVPLIYVTAQAQKFLTLTTCRKLGLADIDYT 304
QY 304 PINNEHLAKKESEFRVNIPLTSTFSPNTEKAGSDKAKIIMEAKPGYALVGFELSK 363
DB 305 SIMNEHLAKKESEFRVNIPLTSTFSPNTEKAGSDKAKIIMEAKPGYALVGFELSK 364
QY 364 DSIAVLKYYQAKLKNATQIDKDSISEIYVGIDIKLCPDQSEQMYTNKIAFPNBYITK 423
DB 365 DSIAVLKYYQAKLKNATQIDKDSISEIYVGIDIKLCPDQSEQMYTNKIAFPNBYITK 424

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QY 424 IAPTKLNSLRVEYLANPYDSSDGDIDINKKRISSSEAPFSMANNNDGYMPTGISFT 483
DB 425 IDFTKMKTLRLRYEVLANPYDSSDGTETIDINKKRVSSSEAPFRTLSDNDGVYMPGLVISFT 484
QY 484 FLTPINGFGLVVDENSRILVTLTCKSYLRETLATDLSKREKLIYPPNGFISNIYENGNI 543
DB 485 FLTPINGFGLQADENSRILITLCKSYLRELLATDLSKREKLIYPPNGFISNIYENGSI 544
QY 544 EGENLEPWKANNKAAVVDHTGCVNGTKVLYVHEDGEPFQITGDKLKLTREYVIOYIVGK 603
DB 545 EEDNLEPWKANNKAAVVDHTGCVNGTKVLYVHEDGEPFQITGDKLKLTREYVIOYIVGK 604
QY 604 AAIYKDEKNGDYIYEEENNELEDPQAVTKRPIGTDSRPHLFTSQNGSEARCGNFI 663
DB 605 PSILKDEKNTYIHYEDTNMNLKDYQITTKRFTYGTDLKGVYLLIKSQNGDEAWGDKFTI 664
QY 664 SEIRPSEELSPELIKSDAWGSGQWISGNSLINSVNGTFRONTLSAESYTSNMFN 723
DB 665 LEIKPAEDLSPELINRSMWITTPGASISGNKLIINLGTNGTFRQSLINSYSTISFT 724
QY 724 VNGFGKVTIRNSREVEREVSYLQPSKYSKFTTTTNTGELYELSRAS-SRGVINGD 782
DB 725 ASGPFNVTVRNSREVLFRSVLMSTSHISGTFPTESNNTGLVYELSRSGGGHISPN 784
QY 783 FSIK 786
DB 785 VSIK 788
RESULT 9
ADN08753
ID ADN08753 standard; protein; 788 AA.
AC ADN08753;
XX
DT 17-JUN-2004 (first entry)
XX
DE B. thuringiensis vip3c SEQ ID NO:2.
XX
KM vip3c; toxin; protease inhibitor; lepidopteran; tobacco budworm;
KM sunflower head moth; beet armyworm; insect-resistance; maize.
XX
OS Bacillus thuringiensis.
XX
FH Key Location/Qualifiers
FT Misc-difference 738
FT /label= Glu, Gly
XX
PN WO2003075655-A2.
XX
PD 18-SEP-2003.
XX
PF 20-FEB-2003; 2003WO-US004735.
XX
PR 06-MAR-2002; 2002US-0362250P.
XX
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
PI Shen Z, Warren GW, Shothoski F, Kramer V;
XX
DR WPI; 2003-788166/74.
DR N-PSDB; ADN08752, ADN08754.
XX
XX New Vip3 toxin encoded by a nucleic acid from Bacillus thuringiensis,
PT useful for controlling lepidopteran insects such as tobacco budworm,
PT sunflower head moth or beet armyworm, or for producing an insect-
PT resistant transgenic plant.
XX
PS Claim 59; SEQ ID NO 2; 118bp; English.
XX
CC The invention relates to a novel isolated Vip3 toxin that is active
CC against insects. The toxin acts as a protease inhibitor. The Vip3 toxin,

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CC hybrid toxin and nucleic acid molecules are useful for controlling
CC lepidopteron insects such as tobacco budworm, sunflower head moth or beet
CC armyworm, for producing an insect-resistant transgenic plant, and
CC protecting a maize plant against at least one insect pest. The present
CC sequence represents native B. thuringiensis vip3c.

XX
SQ Sequence 788 AA;

Query Match 81.1%; Score 3239; DB 7; Length 788;
Best Local Similarity 80.7%; Pred. No. 1.9e-190;
Matches 636; Conservative 64; Mismatches 86; Indels 2; Gaps 2;

QY 1 MOKNN-KLSVKALPSFIDYFNGIYGFATGIDIMNMIFFKNTGGDLTLDLILKNQQLANE 59
DB 1 MNKNNTKLSSTRALPSFIDYFNGIYGFATGIDIMNMIFFKNTGGDLTLDLILKNQQLANE 60
QY 60 ISGKLDGVNGSLNDLLAOGNLDTLSEIKELIKIANEQVLDVNNKLDALNTMLTYLPK 119
DB 61 ISGKLDGVNGSLNDLLAOGNLDTLSEIKELIKIANEQVLDVNNKLDALNTMLTYLPK 120
QY 120 ITSMUSDVKNQVYALGLOIEYLSKQLEISDKLDVINNVVLIINSTLTETTPAYQRIKYVN 179
DB 121 ITSMUSDVKNQVYALGLOIEYLSKQLEISDKLDVINNVVLIINSTLTETTPAYQRIKYVN 180
QY 180 EKFEALTSATEENLTKTKODSSHTDILDELTELTELAKSVTKNDVDFEFLNTFHDVMIG 239
DB 181 EKFEALTSATEENLTKTKODSSHTDILDELTELTELAKSVTKNDVDFEFLNTFHDVMIG 240
QY 240 NNLFGRSALKTASELILAKENLTKSGSEVGVNVPFLIVLTALQAKAFLLTTCRKLGLAD 299
DB 241 NNLFGRSALKTASELILAKENLTKSGSEVGVNVPFLIVLTALQAKAFLLTTCRKLGLAD 300
QY 300 IDYTPIMNEHLNKEKEEFRVNIPLTSLNTPSNPNYEKARGSDKDAKIIMEAKPGYALVGF 359
DB 301 IDYTPIMNEHLNKEKEEFRVNIPLTSLNTPSNPNYEKARGSDKDAKIIMEAKPGYALVGF 360
QY 360 ELSKDSIAYLKYQALQKANYQIDKQSLSLIYVGDIDKLCIPQOSEQMYTNTKIAPNEXY 419
DB 361 ELSKDSIAYLKYQALQKANYQIDKQSLSLIYVGDIDKLCIPQOSEQMYTNTKIAPNEXY 420
QY 420 VITKIAFTKKNLSRYEVTANFYDSSTGDIIDLNKKKIESEAFSLMNNNDVWPIGR 479
DB 421 VITKIDFTKMKTLKRYEVTANFYDSSTGDIIDLNKKKIESEAFSLMNNNDVWPIGR 480
QY 480 ISETFLTPINGFGLVVDENSRLVTLTCKSYLRETLATDLSNKEKLIIVPPNGFISNIYE 539
DB 481 ISETFLTPINGFGLVVDENSRLVTLTCKSYLRETLATDLSNKEKLIIVPPNGFISNIYE 540
QY 540 NGNLEGENLEPWKANNKNAIVDHTGVNGTKVLVYHEDGFSQFIDDKLKATEYVIQYT 599
DB 541 NGNLEGENLEPWKANNKNAIVDHTGVNGTKVLVYHEDGFSQFIDDKLKATEYVIQYT 600
QY 600 VNGKAIYLVKDEKNGDIYIEETNNELEDQAVTKRITGTDGSRVHLITPSQNGEARPG 659
DB 601 VNGKPSIHLKDEKNTYGIHYEDTNLNDKDYQYITKRTTGTDLKGVLLILKSQGDAAWED 660
QY 660 NFILISEIRSEBELISPELIRKSDAVGSOQTWISGNSIANSVNGTFRONLSLESYSTYS 719
DB 661 KETLIEIKDAEDLISPELINPNSWITTPASISGNLFINLGNNGFRGSLSIANSYSTYS 720
QY 720 MNFNNVNGRKYTIRNSREYVFERASYIQFSSKYSIEKFTTTNNNTGGLVVELSRAS-SRGVY 778
DB 721 ISFTISGPFNVYVRSRYLVLFERSNIMSSSTSHISGTFKTESNNTGLVVELSRSGGGGHI 780
QY 779 NFGDFSIX 786
DB 781 SPENVSIX 788

RESULT 10
ADN08762
ID ADN08762 standard; protein; 788 AA.

AC ADN08762;
XX 17-JUN-2004 (first entry)
DT XX
DE B. thuringiensis vip3A-C fusion protein SEQ ID NO:11.
XX vip3c; toxin; protease inhibitor; lepidopteron; tobacco budworm;
KM sunflower head moth; beet armyworm; insect-resistance; maize; vip3A-C.
XX
OS Bacillus thuringiensis.
OS Chimeric.
XX WO2003075655-A2.
PN 18-SEP-2003.
PD 20-FEB-2003; 2003WO-US004735.
PF 06-MAR-2002; 2002US-0362250P.
PR (SYGN) SYNGENTA PARTICIPATIONS AG.
PA Shen Z, Warren GW, Shockoski F, Kramer V;
PI WPI; 2003-788166/74.
XX DR N-PSDB; ADN08761.
XX PT New Vip3 toxin encoded by a nucleic acid from Bacillus thuringiensis,
PT useful for controlling lepidopteran insects such as tobacco budworm,
PT sunflower head moth or beet armyworm, or for producing an insect-
PT resistant transgenic plant.
XX
PS Claim 12; SEQ ID NO 11; 118pp; English.
XX
CC The invention relates to a novel isolated Vip3 toxin that is active
CC against insects. The toxin acts as a protease inhibitor. The Vip3 toxin,
CC hybrid toxin and nucleic acid molecules are useful for controlling
CC lepidopteron insects such as tobacco budworm, sunflower head moth or beet
CC armyworm, for producing an insect-resistant transgenic plant, and
CC protecting a maize plant against at least one insect pest. The present
CC sequence represents vipA-C, a B. thuringiensis vip3A-vip3C fusion
CC protein.
XX
SQ Sequence 788 AA;

Query Match 81.0%; Score 3235; DB 7; Length 788;
Best Local Similarity 80.5%; Pred. No. 3.3e-190;
Matches 634; Conservative 64; Mismatches 88; Indels 2; Gaps 2;

QY 1 MOKNN-KLSVKALPSFIDYFNGIYGFATGIDIMNMIFFKNTGGDLTLDLILKNQQLANE 59
DB 1 MNKNNTKLSSTRALPSFIDYFNGIYGFATGIDIMNMIFFKNTGGDLTLDLILKNQQLANE 60
QY 60 ISGKLDGVNGSLNDLLAOGNLDTLSEIKELIKIANEQVLDVNNKLDALNTMLTYLPK 119
DB 61 ISGKLDGVNGSLNDLLAOGNLDTLSEIKELIKIANEQVLDVNNKLDALNTMLTYLPK 120
QY 120 ITSMUSDVKNQVYALGLOIEYLSKQLEISDKLDVINNVVLIINSTLTETTPAYQRIKYVN 179
DB 121 ITSMUSDVKNQVYALGLOIEYLSKQLEISDKLDVINNVVLIINSTLTETTPAYQRIKYVN 180
QY 180 EKFEALTSATEENLTKTKODSSHTDILDELTELTELAKSVTKNDVDFEFLNTFHDVMIG 239
DB 181 EKFEALTSATEENLTKTKODSSHTDILDELTELTELAKSVTKNDVDFEFLNTFHDVMIG 240
QY 240 NNLFGRSALKTASELILAKENLTKSGSEVGVNVPFLIVLTALQAKAFLLTTCRKLGLAD 299
DB 241 NNLFGRSALKTASELILAKENLTKSGSEVGVNVPFLIVLTALQAKAFLLTTCRKLGLAD 300
QY 300 IDYTPIMNEHLNKEKEEFRVNIPLTSLNTPSNPNYEKARGSDKDAKIIMEAKPGYALVGF 359
DB 301 IDYTPIMNEHLNKEKEEFRVNIPLTSLNTPSNPNYEKARGSDKDAKIIMEAKPGYALVGF 360

QY 360 EISKDSIAVLKVTYQAKLKHNYQIDKSLSEIYVGDIDKLCPPDSEQWYTTNKIAFPNEY 419
CC EISNDSTIVLKVEBAKQKQYQVDKDSISEVITYGDMOKLCPDQSEQIYYTNNIVFPNEY 420
Db 361 EISNDSTIVLKVEBAKQKQYQVDKDSISEVITYGDMOKLCPDQSEQIYYTNNIVFPNEY 420
QY 420 VITKIAFTKRLNSLRVETANFYDSSGTGDDIDLNKKKIESSPAEFSMANNDGVYMPIGT 479
Db 421 VITKIDFTKQKKTILRYEVTANFYDSSGTGIDLNKKKIESSPAEFRTLSANDGVYMPIGV 480
QY 480 ISEFELPPIINGFGLVVDENSRILVTLCYSYARETLATDLSNKKETKLIYPNGFISNIIVE 539
Db 481 ISEFELPPIINGFGLVVDENSRILVTLCYSYARETLATDLSNKKETKLIYPNGFISNIIVE 540
QY 540 NGNLEGENLEBPWKANNKNAAYVDHTGAVNGTKVLYVHEDEFSQFIDGKLKLTETVYIQT 599
Db 541 NGNLEGENLEBPWKANNKNAAYVDHTGAVNGTKVLYVHEDEFSQFIDGKLKLTETVYIQT 600
QY 600 VKGKAALYLKDEKNGDYIYEETNNLEDPQAVTKRFTTGDSRVHLIFTSQNGEBAFG 659
Db 601 VKGKPSIHLKDEKNGDYIHYEDTNNNLEDPQAVTKRFTTGDTLKGAVYILKQNGDEAMGD 660
QY 660 NFIISERPEBELISPELISDAVWGSGTWMISGNSLNINSNVNCTFRQMLSESYSTYS 719
Db 661 KFTILETKPADDLSPBLINPNSWITTPGASISGNKLPINLGTNGTRQSLSNSYSTYS 720
QY 720 MNFVNGFGKVTIRNSREVVERSYLOFSSKYISEKFTTTNNGLYVELSRAS-SRGVI 778
Db 721 ISFPAEPFVNTVYANSRGVLFERSNLSMSTSHISGTIKTESNNTGLVELSRSGGGHI 780
QY 779 NFGDPSIK 786
Db 781 SFENVSIK 788

RESULT 11
AAW46862
ID AAW46862 standard; protein; 789 AA.
XX
XX AAW46862;
DT 11-JUN-1998 (first entry)
XX
XX Bacillus thuringiensis toxin designated 86Bb1(c).
KM Toxin; lepidopteran pest; control; Agrotis ipsilon; black cutworm;
KM Heliothis virescens; Helicoverpa zea.
OS Bacillus thuringiensis.
XX
XX WO9800546-A2.
PN
XX
XX 08-JAN-1998.
PD
XX
XX 01-JUL-1997; 97MO-US011658.
PF
XX
XX 01-JUL-1996; 96US-00674002.
PR
XX
XX (MYCO) MYCOGEN CORP.
PA
XX
XX Schmepef HE, Wicker C, Narva KE, Walz M, Stockhoff BA;
PI
XX
XX WPI; 1998-086971/08.
DR
XX
XX N-PSDB; AAV16521.
PT
XX
XX New isolated Bacillus thuringiensis isolate(s) - used to obtain genes
PT encoding toxins which are active against lepidopteran pests such as the
PT Black cutworm.
PS
XX
XX Claim 42; Page 117-120; 183pp; English.
CC
XX
XX The present sequence represents a Bacillus thuringiensis toxin which is
CC active against lepidopteran pests. The toxin isolates can be used for the
CC control of lepidopteran pests such as Agrotis ipsilon (black cutworm),
CC Heliothis virescens and Helicoverpa zea. PCR primers and probes can be

CC derived from the polynucleotide encoding the toxin and used for the
CC amplification and detection of other toxin-encoding sequences
XX
XX Sequence 789 AA;
Query Match 79.7%; Score 3182.5; DB 2; Length 789;
Best Local Similarity 79.0%; Pred. No. 5.7e-187;
Matches 624; Conservative 69; Mismatches 92; Indels 5; Gaps 3;
QY 1 MOKN-KLSYKALPSFIDYNGYGFATGDKDMMNMFKNNTGSDTLDELTKNQOLNE 59
Db 1 MNKNNTKLSYKALPSFIDYNGYGFATGDKDMMNMFKNNTGSDTLDELTKNQOLNE 60
QY 60 ISGCLDGVNGLNDLDAQNLDELSEKILKINEOKVLYNDVTKDAITMLNTYLPK 119
Db 61 ISGCLDGVNGLNDLDAQNLDELSEKILKINEOKVLYNDVTKDAITMLNTYLPK 120
QY 120 ITSMLSQVMDKONVALGLQIEYLSKQLEISDKLDVINNVNLINSTLTPAYORIKYVN 179
Db 121 ITSMLSQVMDKONVALGLQIEYLSKQLEISDKLDVINNVNLINSTLTPAYORIKYVN 180
QY 180 EKFEALTSATETMLKTKQDSSHDDIDELTELTELAKSVTKNDVGDGEFFIANTHDVWG 239
Db 181 EKFEALTSATETMLKTKQDSSHDDIDELTELTELAKSVTKNDVGDGEFFIANTHDVWG 240
QY 240 NNLFGSRLATASRLAKENLKTSGSERGVNVPFLYLTALQAKFLTLTCRKLGLAD 299
Db 241 NNLFGSRLATASRLAKENLKTSGSERGVNVPFLYLTALQAKFLTLTCRKLGLAD 300
QY 300 IDYTPINNEHLNKEKEFRVNLPTLSNTPSNRYEVARGSDDKAKIMEAKPGYALVGF 359
Db 301 IDYTPINNEHLNKEKEFRVNLPTLSNTPSNRYEVARGSDDKAKIMEAKPGYALVGF 360
QY 360 EISKDSIAVLKVTYQAKLKHNYQIDKSLSEIYVGDIDKLCPPDSEQWYTTNKIAFPNEY 419
Db 361 EISNDSTIVLKVEBAKQKQYQVDKDSISEVITYGDMOKLCPDQSEQIYYTNNIVFPNEY 420
QY 420 VITKIAFTKRLNSLRVETANFYDSSGTGDDIDLNKKKIESSPAEFSMANNDGVYMPIGT 479
Db 421 VITKIDFTKQKKTILRYEVTANFYDSSGTGIDLNKKKIESSPAEFRTLSANDGVYMPIGV 480
QY 480 ISEFELPPIINGFGLVVDENSRILVTLCYSYARETLATDLSNKKETKLIYPNGFISNIIVE 539
Db 481 ISEFELPPIINGFGLVVDENSRILVTLCYSYARETLATDLSNKKETKLIYPNGFISNIIVE 540
QY 540 NGNLEGENLEBPWKANNKNAAYVDHTGAVNGTKVLYVHEDEFSQFIDGKLKLTETVYIQT 599
Db 541 NGNLEGENLEBPWKANNKNAAYVDHTGAVNGTKVLYVHEDEFSQFIDGKLKLTETVYIQT 600
QY 600 VKGKAALYLKDEKNGDYIYEETNNLEDPQAVTKRFTTGDSRVHLIFTSQNGEBAFG 659
Db 601 VKGKPSIHLKDEKNGDYIHYEDTNNNLEDPQAVTKRFTTGDTLKGAVYILKQNGDEAMGD 660
QY 660 NFIISERPEBELISPELISDAVWGSGTWMISGNSLNINSNVNCTFRQMLSESYSTYS 719
Db 661 NFIISERPEBELISPELISDAVWGSGTWMISGNSLNINSNVNCTFRQMLSESYSTYS 720
QY 720 MNFVNGFGKVTIRNSREVVERSYLOFSSKYISEKFTTTNNGLYVELSRAS--RG 776
Db 721 VYFVSQGDANVRIANSREVLFEKRYMS-GAKDVESEMTTFEKKDNFYIELSQNNLYGCP 779
QY 777 VINRGPSTIK 786
Db 780 IYHNDVSIK 789

RESULT 12
AAV24965
ID AAV24965 standard; protein; 789 AA.
XX
XX AAV24965;
DT 09-SEP-1999 (first entry)

```

XX DE Bacillus thuringiensis toxin 86Bb1 (c).
XX KM Bacillus thuringiensis toxin; Ostrinia nubilalis; lepidopteran;
XX KM European corn borer; black cutworm.
XX OS Bacillus thuringiensis.
XX PN MO9933991-A2.
XX PD 08-JUL-1999.
XX PF 15-DEC-1998; 98MO-US026585.
XX PR 31-DEC-1997; 97US-00002285.
XX PA (MYCO ) MYCOGEN CORP.
XX PI Schnepf HE, Wicker C, Narva KE, Walz M, Stockhoff BA;
XX PI Muller-Cohn J;
XX DR MPI; 1999-40513/34.
XX DR N-PSDB; AAX83882.
XX PT Method for control of European corn borer using Bacillus thuringiensis
XX PT toxins.
XX PS Claim 1; Page 121-124; 174pp; English.
XX CC A method has been developed for the control of European corn borer
XX CC (Ostrinia nubilalis), comprising contacting the pest with a pesticidal
XX CC amount of a Bacillus thuringiensis toxin. The method is used for the
XX CC control of European corn borer (Ostrinia nubilalis). The method can also
XX CC be used for the control of other non-mammalian pests, particularly black
XX CC cutworm, and other lepidopteran pests. The present sequence represents a
XX CC Bacillus thuringiensis toxin from the present invention
XX SQ Sequence 789 AA;

Query Match          79.7%; Score 3182.5; DB 2; Length 789;
Best Local Similarity 79.0%; Pred. No. 5.7e-187;
Matches 624; Conservative 69; Mismatches 92; Indels 5; Gaps 3;

QY 1 MOKNN-KLSVKALPSFDYFNIGYGFATGKIDIMNMIKTNNGDITLDELINNOOLNE 59
DB 1 MNKNNTKLSFTRALPSFDYFNIGYGFATGKIDIMNMIKTDTCGNLTLDIILNNOOLNE 60
QY 60 ISGKLDGVNGSLNDLILAOGNLDTLSEKELIKINEQNKYLANDVNTKDALINMLNTYLPK 119
DB 61 ISGKLDGVNGSLNDLILAOGNLDTLSEKELIKIANEQNOVANDVNNKLDLINTMLATYLPK 120
QY 120 ITSMLSDWKKNYALGLQIEYLSKQKEISDKLDVINNVNLINSTLTETTPAYQRIKYVN 179
DB 121 ITSMLSDWKKNYALGLQIEYLSKQKEISDKLDIINNVNLINSTLTETTPAYQRIKYVN 180
QY 181 EKFEELTPTAETETTLKVKDSSPADIIDELTELTELAKSVTKNDVDSEFEFLTNFHDVWG 240
DB 180 EKFEALTSATEINLTKKQDSSHTDILDELTELTELAKSVTKNDVDSEFEFLTNFHDVWG 239
QY 240 NNLFSGSALKTASELAKENLKTSGSEGVGNVNFLLVLRLOAKALTLTTCKKLGLAD 299
DB 241 NNLFSGSALKTASELAKENLKTSGSEGVGNVNFLLVLRLOAKALTLTTCKKLGLAD 300
QY 300 IDVTPTMNEHLNKEKEFRVNIPLTSLNTFSNPNYKARGSDADAKIMEAKPGYALVGP 359
DB 301 IDVTPTMNEHLNKEKEFRVNIPLTSLNTFSNPNYKARGSDADAKIMEAKPGYALVGP 360
QY 360 EISKDSIALVKYQAKLKNNYQIDKDSLEIYVGDIDKLLCPDQSEOMYTNKIAFPNEY 419
DB 361 EMSNDSITVLKYEAALKQNYQVDKDSLEIYVGDIDKLLCPDQSEOMYTNKIAFPNEY 420
QY 420 VTTKLAFTCKKSLRVEVTANPFDSSTGDIIDAKKKIJSSESEAFSLMANNNDGVYMPDGT 479
DB 420 VTTKLAFTCKKSLRVEVTANPFDSSTGDIIDAKKKIJSSESEAFSLMANNNDGVYMPDGT 479

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DB 421 VITKIDFTKMMKTLRYEVTANPFYDSSSTGEIDLNKKKVESESEAEYRTLSANDGDVMPDGV 480
QY 480 ISFTPLTPINGPGLVVDENSRVLVTLCKSYLRRETLATDLSNKEPTLIYPPNPFISNIVE 539
DB 481 ISFTPLTPINGPGLVVDENSRVLVTLCKSYLRRETLATDLSNKEPTLIYVPSGPFISNIVE 540
QY 540 NGNLAGENLEPMWRANKNNAVVDHTGCVNGTKVLYVHEDGFSQFIDKLLAKTEYVYQYI 599
DB 541 NGNLAGENLEPMWRANKNNAVVDHTGCVNGTKVLYVHEDGFSQFIDKLLAKTEYVYQYI 600
QY 600 VKGKAAIYLKDEKNGYIYIETNNELEDFOATVTRFTTGTDSRVLHIFTSONGEAPFG 659
DB 601 VKGKPSIHLKDEKNGYIYIETNNELEDFOATVTRFTTGTDSRVLHIFTSONGEAPFG 660
QY 660 NFIISIRPSEELISPELTKSDAWGSGQWTISGNSLNINSNVNGTFRONLSIESYSTVS 719
DB 661 NFIILISIRPSEELISPELTKSDAWGSGQWTISGNSLNINSNVNGTFRONLSIESYSTVS 720
QY 720 MNEVNGPFGKVTIRNSREVFEKSYLQFSKXVISEKFTYTYNTGCVYVELSRAS--RG 776
DB 721 VYFSVSGDANVRIRNSREVFEKRYMS-GAKDVSSEMTTKFEKDNFYIELSGGNLYGCP 779
QY 777 VINFGDPSTIK 786
DB 780 IVHFNDVSIX 789

RESULT 13
AAM46863
ID AAM46863 standard; protein; 789 AA.
XX AC AAM46863;
XX AC 11-JUN-1998 (first entry)
XX DT 11-JUN-1998 (first entry)
XX DE Bacillus thuringiensis toxin designated 86V1(a).
XX KM Toxin; lepidopteran pest; control; Agrotis ipsilon; black cutworm;
XX KM Heliothis virescens; Helicoverpa zea.
XX OS Bacillus thuringiensis.
XX PN MO9800546-A2.
XX PD 08-JAN-1998.
XX PF 01-JUL-1997; 97MO-US011658.
XX PR 01-JUL-1996; 96US-00674002.
XX PA (MYCO ) MYCOGEN CORP.
XX PI Schnepf HE, Wicker C, Narva KE, Walz M, Stockhoff BA;
XX PI MPI; 1998-086971/08.
XX DR N-PSDB; AAV16522.
XX PT New isolated Bacillus thuringiensis isolate(s) - used to obtain genes
XX PT encoding toxins which are active against lepidopteran pests such as the
XX PT black cutworm.
XX PS Claim 42; Page 122-126; 183pp; English.
XX CC The present sequence represents a Bacillus thuringiensis toxin which is
XX CC active against lepidopteran pests. The toxin isolates can be used for the
XX CC control of lepidopteran pests such as Agrotis ipsilon (black cutworm),
XX CC Heliothis virescens and Helicoverpa zea. PCR primers and probes can be
XX CC derived from the polymucleotide encoding the toxin and used for the
XX CC amplification and detection of other toxin-encoding sequences
XX SQ Sequence 789 AA;

Query Match          79.6%; Score 3180.5; DB 2; Length 789;

```

Best Local Similarity 78.9%; Pred. No. 7.5e-187;
Matches 623; Conservative 70; Mismatches 92; Indels 5; Gaps 3;

```

QY 1 MOKNN-KLSVAKLPSFDYNGIYGPAFGIDIMNMIFKTMGTGDLTLDLILKNOQLNE 59
DB 1 MANKNTKLSARALPSFDYNGIYGPAFGIDIMNMIFKTMGTGDLTLDLILKNOQLNE 60
QY 60 ISGLDGVNGSLNDLLAOGNLDTELSKEILKIANEQNVKLVNDVNTKLDAINMLNTYLPK 119
DB 61 ISGLDGVNGSLNDLLAOGNLDTELSKEILKIANEQNVKLVNDVNTKLDAINMLNTYLPK 120
QY 120 ITSMUSDVWKONYALGLQIEYLSKQLEISDKLDIVINNVTLNSTLTETPAYORIKYVN 179
DB 121 ITSMUSDVWKONYALGLQIEYLSKQLEISDKLDIVINNVTLNSTLTETPAYORIKYVN 180
QY 180 EKEPALTSATEMTKTKODSSHDDILDELTELTELAKSVTKNDVDGEFFYANTFHDVMIG 239
DB 181 EKEBELTPATEYTSKVKKDSPPADILDELTELTELAKSVTKNDVDGEFFYANTFHDVMIG 240
QY 240 NNLFGRSALKTASELLAKENIKTSGSEVGNVNFILVLTALQAKAFLLTTCRKLGLAD 299
DB 241 NNLFGRSALKTASELLAKENIKTSGSEVGNVNFILVLTALQAKAFLLTTCRKLGLAD 300
QY 300 IDYTPIMNEHLNKEKEEFRVNIILPTLSNTEFSNPNYERKARGSDKDAKIMEAKPGYALVGF 359
DB 301 IDYTSIMNEHLNKEKEEFRVNIILPTLSNTEFSNPNYERKARGSDKDAKIMEAKPGYALVGF 360
QY 360 EISKDSIALVKYQAKLKANYQIDKDSLSIYVGDIDKLCPDQSEQMTYTNKIAFPNEY 419
DB 361 EMSNDSITVLKYVEAKLKONYQVDKDSLSIYVGDIDKLCPDQSEQMTYTNKIAFPNEY 420
QY 420 VITKIAFTKGLNSLRYEVTANFYDSSTGDDIDLNKKKIESSEAFSPMLNANDGVYMPIGT 479
DB 421 VITKIDFTKGLKTLRIEVTANFYDSSSTGEIDLNKKKIESSEAFSPMLNANDGVYMPIGT 480
QY 480 ISETFLTPINGFGLVNDENSRVLTLCCKSYLRETLATDLSNKEKTLIVPNSGFISNIYE 539
DB 481 ISETFLTPINGFGLVNDENSRVLTLCCKSYLRETLATDLSNKEKTLIVPNSGFISNIYE 540
QY 540 NGNLEGNLEBPWKANNNAAYVDHTGCVNGTAVLYVHEDGERSOFIDGKALKATEYVQYI 599
DB 541 NGNLEGNLEBPWKANNNAAYVDHTGCVNGTAVLYVHEDGERSOFIDGKALKATEYVQYI 600
QY 600 VKGKAALYLDKDEKNGDIYEETNNLEDFQAVTRFTITGDSRVHLIFTSQNGEBAFG 659
DB 601 VKGKPSIHLKDENGYIHYEDTNNNLADYQITIRFTTGTDLKGVYILKSQNGDEAKGD 660
QY 660 NFIISEIRPSEBELISPELLIKSDAVVSGQGTWISGNSLINSNVNVTFRONLSLESYSTYS 719
DB 661 NFIISEIRPSEBELISPELLIKSDAVVSGQGTWISGNSLINSNVNVTFRONLSLESYSTYS 720
QY 720 MNFRNVGFGKVTIRNSREVVPERSYLOPSSKYISEKTTTNTNTGLYVEISRASS--RG 776
DB 721 VYFVSQSDANVVRIRNSREVLFEKGYMS-GAKDVSEMTTYREKDNFYIELSQGNLYGCP 779
QY 777 VINFGDESIK 786
DB 780 IVHFYDVSIK 789

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RESULT 14

AAV24966 standard; proteln: 789 AA.

AAV24966;

09-SBP-1999 (first entry)

Bacillus thuringiensis toxin 86v1 (a).

Bacillus thuringiensis; toxin; Oestrinia nubilalis; lepidopteran;

European corn borer; black cutworm.

OS Bacillus thuringiensis.

XX W09933991-A2.

XX 08-JUL-1999.

PF 15-DEC-1998; 98WO-US026585.

PR 31-DEC-1997; 97US-00002285.

FA (MYCO) MYCOGEN CORP.

PI Schepf HE, Wicker C, Narva KE, Walz M, Stockhoff BA;

PI Muller-Cohn J;

XX WP1, 1999-405513/34.

DR N-PSDB; AAX831883.

PT Method for control of European corn borer using Bacillus thuringiensis

PS toxins.

XX Claim 1, Page 126-129, 17app, English.

CC A method has been developed for the control of European corn borer

CC (Oestrinia nubilalis), comprising contacting the pest with a pesticidal

CC amount of a Bacillus thuringiensis toxin. The method is used for the

CC control of European corn borer (Oestrinia nubilalis). The method can also

CC be used for the control of other non-mammalian pests, particularly black

CC cutworm, and other lepidopteran pests. The present sequence represents a

CC Bacillus thuringiensis toxin from the present invention

XX

SO Sequence 789 AA;

Query Match 79.6%; Score 3180.5; DB 2; Length 789;

Best Local Similarity 78.9%; Pred. No. 7.5e-187;

Matches 623; Conservative 70; Mismatches 92; Indels 5; Gaps 3;

```

QY 1 MOKNN-KLSVAKLPSFDYNGIYGPAFGIDIMNMIFKTMGTGDLTLDLILKNOQLNE 59
DB 1 MANKNTKLSARALPSFDYNGIYGPAFGIDIMNMIFKTMGTGDLTLDLILKNOQLNE 60
QY 60 ISGLDGVNGSLNDLLAOGNLDTELSKEILKIANEQNVKLVNDVNTKLDAINMLNTYLPK 119
DB 61 ISGLDGVNGSLNDLLAOGNLDTELSKEILKIANEQNVKLVNDVNTKLDAINMLNTYLPK 120
QY 120 ITSMUSDVWKONYALGLQIEYLSKQLEISDKLDIVINNVTLNSTLTETPAYORIKYVN 179
DB 121 ITSMUSDVWKONYALGLQIEYLSKQLEISDKLDIVINNVTLNSTLTETPAYORIKYVN 180
QY 180 EKEPALTSATEMTKTKODSSHDDILDELTELTELAKSVTKNDVDGEFFYANTFHDVMIG 239
DB 181 EKEBELTPATEYTSKVKKDSPPADILDELTELTELAKSVTKNDVDGEFFYANTFHDVMIG 240
QY 240 NNLFGRSALKTASELLAKENIKTSGSEVGNVNFILVLTALQAKAFLLTTCRKLGLAD 299
DB 241 NNLFGRSALKTASELLAKENIKTSGSEVGNVNFILVLTALQAKAFLLTTCRKLGLAD 300
QY 300 IDYTPIMNEHLNKEKEEFRVNIILPTLSNTEFSNPNYERKARGSDKDAKIMEAKPGYALVGF 359
DB 301 IDYTSIMNEHLNKEKEEFRVNIILPTLSNTEFSNPNYERKARGSDKDAKIMEAKPGYALVGF 360
QY 360 EISKDSIALVKYQAKLKANYQIDKDSLSIYVGDIDKLCPDQSEQMTYTNKIAFPNEY 419
DB 361 EMSNDSITVLKYVEAKLKONYQVDKDSLSIYVGDIDKLCPDQSEQMTYTNKIAFPNEY 420
QY 420 VITKIAFTKGLNSLRYEVTANFYDSSTGDDIDLNKKKIESSEAFSPMLNANDGVYMPIGT 479
DB 421 VITKIDFTKGLKTLRIEVTANFYDSSSTGEIDLNKKKIESSEAFSPMLNANDGVYMPIGT 480
QY 480 ISETFLTPINGFGLVNDENSRVLTLCCKSYLRETLATDLSNKEKTLIVPNSGFISNIYE 539
DB 481 ISETFLTPINGFGLVNDENSRVLTLCCKSYLRETLATDLSNKEKTLIVPNSGFISNIYE 540

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QY 540 NGNLEGENLEPMKANNKNAAYVDHTGVNGTKVLYVHEDGEFSQFIQDKLKLKTEYVIOYI 599
DB 541 NGSIEEDNLEPMKANNKNAAYVDHTGVNGTKVLYVHEDGEFSQFIQDKLKLKTEYVIOYI 600
QY 600 VKKKAIIYLKDEKNGDYIYEETNNELEDFOAVTKRFTTGTDSRYHLIFTSQNGEBAFG 659
DB 601 VKKPSIHLKDEKNGDYIYEETNNELEDFOAVTKRFTTGTGTDLKGVYLLIKSQNGDEAWGD 660
QY 660 NFIISIRPSEELLSPELIKSDAWGSGOTWISGNSINNSVNGTFRONLSIESYSTS 719
DB 661 NFIILSISPESEKLSPELINTNNMTSGSTHISGNTLTLYQGGRIKLKQNLQDSFSTR 720
QY 720 MNFNNGFGKVTIRNSREVVFRSYLQFSKXYISEKFTTTNNYGLVVELSRAS--RG 776
DB 721 VYFSVSGDANVIRNSREVLFEKGYMS-GAKOVSEMTTTFEKNDFYIELSGNNLYGCP 779
QY 777 VINFGDPSIK 786
DB 780 IVHFYDVSIK 789

RESULT 15
AAW46867
ID AAW46867 standard; protein; 789 AA.
AC AAW46867;
DT 11-JUN-1998 (first entry)
XX
DE Bacillus thuringiensis toxin designated 2025(a).
XX
KW Toxin; lepidopteran pest; control; Agrotis ipsilon; black cutworm;
KW Heliothis virescens; Helicoverpa zea.
XX
OS Bacillus thuringiensis.
XX
FH Key Location/Qualifiers
FT Misc-difference 97
FT /note= "encoded by AT"
XX
PN WO9800546-A2.
XX
PD 08-JAN-1998.
XX
PF 01-JUL-1997; 97MO-US011658.
XX
PR 01-JUL-1996; 96US-00674002.
XX
PA (MYCO) MYCOGEN CORP.
PI Schepf HE, Wicker C, Narva KE, Walz M, Stockhoff BA;
PI MPI; 1998-086971/08.
DR N-PSDB; AAV16526.
XX
PT New isolated Bacillus thuringiensis isolate(s) - used to obtain genes
PT encoding toxins which are active against lepidopteran pests such as the
PT Black cutworm.
XX
PS Claim 42; Page 139-142; 183pp; English.
XX
CC The present sequence represents a Bacillus thuringiensis toxin which is
CC active against lepidopteran pests. The toxin isolates can be used for the
CC control of lepidopteran pests such as Agrotis ipsilon (black cutworm),
CC Heliothis virescens and Helicoverpa zea. PCR primers and probes can be
CC derived from the polynucleotide encoding the toxin and used for the
CC amplification and detection of other toxin-encoding sequences
XX
SQ Sequence 789 AA;

QY 1 MOKNN-KLSVKALPSFIDYFNNGIYGFATGIKOIMNMI FKTNTGGDLTLDELLKNQOLNE 59
DB 1 MOKNNKLSKRALPSFIDYFNNGIYGFATGIKOIMNMI FKTNTGGDLTLDELLKNQOLNE 60
QY 60 ISGKLDGVNGSLNDLLAOGNLDTLSKEILLKANEONKYLANDVNTKLDANIMLANTYLPK 119
DB 61 ISGKLDGVNGSLNDLLAOGNLDTLSKEILLKANEONKYLANDVNTKLDANIMLANTYLPK 120
QY 120 ITSMISDWKONVALGQIEYLSKQIEISDKLDVANNVNLNSTLTETTPAYORIKYNN 179
DB 121 ITSMISDWKONVALGQIEYLSKQIEISDKLDVANNVNLNSTLTETTPAYORIKYNN 180
QY 180 EKFEALTSATETNLTAKTODSSHTDIDELTELTELAKSVTKODVDGFEFYLNTFHVMTG 239
DB 181 EKFEALTSATETNLTAKTODSSHTDIDELTELTELAKSVTKODVDGFEFYLNTFHVMTG 240
QY 240 NNLFGRSALKTASSELIAKENLKTSGSEGVNPNFLIVLTAQAKAFLTLTTCRKLGLAD 299
DB 241 NNLFGRSALKTASSELIAKENLKTSGSEGVNPNFLIVLTAQAKAFLTLTTCRKLGLAD 300
QY 300 IDYTPIMNEHLNKEKEFEFVNILPTLSNFPSPNPEKAGSDAKIIMEAKRGYALVGF 359
DB 301 IDYTPIMNEHLNKEKEFEFVNILPTLSNFPSPNPEKAGSDAKIIMEAKRGYALVGF 360
QY 360 EISKDSIAVLKYYQAKLKANNYQIDKDSLSEIYVGDIDKLCFPOSQOMTYTNKKIAPPNEX 419
DB 361 EWSNDSITVLKYYEALKQNYQVDKDSLSEIYVGDIDKLCFPOSQOITYTNKIVPNEX 420
QY 420 VITTKIAFTKCLNSLREYVTANFYDSSGTDIDLNKKKIESSSEAFMSMLNANDGVNPICT 479
DB 421 VITTKIDFTKCMKTLIRYEVANFYDSSGTDIDLNKKKIESSSEAFMSMLNANDGVNPICT 480
QY 480 ISETPLTPINGGLVVDENSRVLVTLTCKSYLAETLLATDLSNKKETFLYPPNGFISNIYE 539
DB 481 ISETPLTPINGGLVVDENSRVLVTLTCKSYLAETLLATDLSNKKETFLYPPNGFISNIYE 540
QY 540 NGNLEGENLEPMKANNKNAAYVDHTGVNGTKVLYVHEDGEFSQFIQDKLKLKTEYVIOYI 599
DB 541 NGSIEEDNLEPMKANNKNAAYVDHTGVNGTKVLYVHEDGEFSQFIQDKLKLKTEYVIOYI 600
QY 600 VKKKAIIYLKDEKNGDYIYEETNNELEDFOAVTKRFTTGTDSRYHLIFTSQNGEBAFG 659
DB 601 VKKPSIHLKDEKNGDYIYEETNNELEDFOAVTKRFTTGTGTDLKGVYLLIKSQNGDEAWGD 660
QY 660 NFIISIRPSEELLSPELIKSDAWGSGOTWISGNSINNSVNGTFRONLSIESYSTS 719
DB 661 NFIILSISPESEKLSPELINTNNMTSGSTHISGNTLTLYQGGRIKLKQNLQDSFSTR 720
QY 720 MNFNNGFGKVTIRNSREVVFRSYLQFSKXYISEKFTTTNNYGLVVELSRAS--RG 776
DB 721 VYFSVSGDANVIRNSREVLFEKGYMS-GAKOVSEMTTTFEKNDFYIELSGNNLYGCP 779
QY 777 VINFGDPSIK 786
DB 780 IVHFYDVSIK 789

Search completed: May 15, 2006, 20:39:13
Job time : 192 secs

Query Match 79.5%; Score 3176.5; DB 2; Length 789;
Best Local Similarity 78.9%; Pred. No. 1.3e-186;
Matches 623; Conservative 69; Mismatches 93; Indels 5; Gaps 3;


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Qy 311 NKEKEFRVNIILPTLSNTPSNPNYEKARGS--DKQAK-----IIMEAKPGALVNG 358
Db 383 NKTLDLDFK-----NKEKGLSNKIDETAKENVOALNYSKNLTLETKRY---- 424
Qy 359 T::SKDSIAVLKVQAKLKNY-----QIDKDS-LSEI-VY 392
Db 425 ---NDQINIDNIKEKEAKQNDQFKEHMKTIIPNEMKYQKPSIEIKIMKDFLSKVNKY 480
Qy 393 GDIDKLCPDQSQWYNNKIAFPNEVYITTKIAFKGLANSLEYET-----ANPYDS 445
Db 481 NDFPKV-----YKEKVESEN-----KFTELNKTITVEVSDSEIKKYEKPFDS 524
Qy 446 TGDIDLNKKIIESSAEFSMLNANDGYMPTIGTSETFPINPFGIWDENSLVLT 505
Db 525 KSLINETKKSIEEQQNINLTKVDYIKVCLANTIE-----LITCHNKQYTLK 573
Qy 506 CK-----SYLRET-----LLAID-----LSNKETKLIIPPNGFISNIVENGNLE----- 544
Db 574 DKLNQNIKTITKEIWSIDKIYTDKFPENILTDKKTLETFGTGLSNHESNNKELITPYD 633
Qy 545 -----GENLEPM-----KANNKAYVDHTGVN-----GTYKLVYHEDGEFSQ 582
Db 634 LKALDGKXKXKMLTKQFNEKEKAVEADIKKXVDINKIVSNIEITVTSIVINEDTE--N 691
Qy 583 FIGDKLKLTVEYVIOYIVKGAATYLDKXKGDYIYEFTNNE 624
Db 692 EIGKSIELNNTKVLKVEKXVANTNINKEIKLXDYDFODPKGK 733

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RESULT 2

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B42771
Reticulocyte-binding protein 2 - Plasmodium vivax (fragment)
C/Species: Plasmodium vivax
C/Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 09-Sep-1997
C/Accession: B42771
R/Galinski, M.R.; Medina, C.C.; Ingravallo, P.; Barnwell, J.W.
Cell 69, 1213-1226, 1992
A/Title: A reticulocyte-binding protein complex of Plasmodium vivax merozoites.
A/Reference number: A42771; MUID:92315338; PMID:1617731
A/Accession: B42771
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-1252 <GAL>
A/Cross-references: UNIPARC:UPI000017B645; GB:M88098; NID:g160627; PID:g160628
A/Experimental source: strain Belém, merozoites
A/Genes: RBP2

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Query Match 5.6%; Score 225; DB 2; Length 1252;
Best Local Similarity 22.0%; Pred. No. 0.01;
Matches 172; Conservative 124; Mismatches 269; Indels 218; Gaps 43;

Qy 3 KNNKLSV-----KALPFIYFNGI-----YGPATGIDIMNMIFKNTVGDLTLDEI 50
Db 535 KKKRKYVDITTKSINSTVGNFSSLFNNPDLNQYDFPKNINDYEN----- 578
Qy 51 LKNOQLNIEISGLDGVNGL-----NDLAAQSLDELSELKILKIAN---EONKVLN 100
Db 579 -KMGELIYFBSGLNKISLNLNASENTSDYNSAKTLRLAOKKEKNILNKKSEANFYLR 637
Qy 101 DVNTKLDALNMLN--TYLPKITSM--SDVMKQNYALGQIEYLSKQLEISDKLDVIN 157
Db 638 DVK-KVESFRFIFNNKESLDKINEMIKKEQLTVNEBHG--NVQOLVENIMELVDE----- 689
Qy 158 NVLINSTLTETPAQRIYVNEKEPALTSATENMLTKYKDS--SHTD-----ILD 206
Db 690 -----NNLSDI-----LKOATGKNEIOKITHSTLKKAKATILGHVDSACYGIGIKTP 738
Qy 207 ELTELTEL-----AKSVTKNDV--DGFERYLATFHDVMIIGNNLFGSALKTASE 253
Db 739 ELA-LTELGLAKAKTQAEQLKFKESKNNVLTETENNSKOT--NELDVHKNI--QDAYKALE 794

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Qy 254 LIA-----KENIKTSGSEVGNVNYFLIV-----TALOAK----- 283
Db 795 ILAHSDEIDTKQKSSKLIEMGNQYLVKLVNLNQYKNNKISSIKSGEAVSVKIGNVSKCH 854
Qy 284 AFLTLTTRKRLGLADIDITYPIANHEHLNKEKEEFPVNIILPTLSNTPSNPNYEKARGSDKD 343
Db 855 SELSKYT-----SDKSVDNI IALEKQTELQNIENNSFTQKRTVNSDSLEKIK----- 903
Qy 344 AKIMEAKPGYALVGFELSKDSIAVLKVQAKL-----HNYQDKD-----SLSEL--V 391
Db 904 -----TDFSELKALATLBEENVALASSDNHSHVOSKEPPVNPALSELKE 950
Qy 392 YGIDKLCPDQSQWYNNKIAFPNEVYITTKIAFKTK-----LNSLREYANP-- 441
Db 951 ETDIDSL--NYALDELKKGRTCEVSHYKLIKQVTEIGISDDELINTIEGNVQAYLAYI 1008
Qy 442 ---YDSSTGDI-----DLNKKIIESS-AEFSMLNANDGYMPTIGTSETFPINPFG 492
Db 1009 KQNEEDTVQDVLTLNHEPNTKQVSNHEPTPFDKSNKSEBELTKAV--TDSKTIISKLKGI 1067
Qy 493 LVVDENSLVLTFTCKSYLRETLATDLSNKETKLIIPPNGFISNIVENGNLEGENLEPMK 552
Db 1068 IEVVENTEMNTIESSAKETIALLY--NELKXKTSL-----NEIYQTSN--EYKLOEMK 1116
Qy 553 ANNKAYVDHTGVNGTKVLYVHEDGEFSQF-----IGDKLKLTVEYVIOYIVK 603
Db 1117 -SNADKYID-----VSKIFNTVLDQKSNIVTNGHSINNVDKXKCK-----LOELIDAD 1165
Qy 604 AAIYLDKXKGDYIYE--ETN--NELDEPQAVTR---FITGDSRVHLIFTSQNGEAP 657
Db 1166 SSFTLSIKKFNENIYSHIKTINIGELBOLQOTNKSEHDNVAKHKEXIVHLI-----NRVESL 1221
Qy 658 GGN 660
Db 1222 KGD 1224

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RESULT 3

```

G70163
hypothetical protein BB0512 - Lyme disease spirochete
C/Species: Borrelia burgdorferi (Lyme disease spirochete)
C/Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C/Accession: G70163
R/Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Iathiga, R.; White
son, D.; Peterson, J.; Kexlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugc,
Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roderick, K.; Hatch, B.
Nature 390, 580-586, 1997
A/Authors: Smith, H.O.; Venter, J.C.
A/Title: Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi.
A/Reference number: A70100; MUID:98065943; PMID:9403685
A/Accession: G70163
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-2166 <KLE>
A/Cross-references: UNIPROT:O51465; UNIPARC:UPI00000574E8; GB:AE001153; GB:AE000783; NID
A/Experimental source: strain B31

```

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Query Match 5.2%; Score 208.5; DB 2; Length 2166;
Best Local Similarity 21.5%; Pred. No. 0.12;
Matches 184; Conservative 141; Mismatches 330; Indels 201; Gaps 45;

Qy 3 KNNKLSVALPSPF-----IDYF-----NGIYGFATGIDIMNMIFKNTVGDLTLDE-----IL 51
Db 910 KELKFSISLSYLYLEKIDEPNGQATYSDDL--LQDINHHNKGTRLEENLSKFAAVL 968
Qy 52 KQ-QQLNIEISGLDGVNGL--NDLAAQSLDELSELKILKIANQNKVLANVNTKLDALN 110
Db 969 NNSSEFVKEVNSLQDKRTDIASF--QANIDITDSLNVK--NDINK--EINGKNEVI 1022
Qy 111 LMLNTYLPKITSM--SDVMKQNYALGQIEYLSKQLEISDKLDVINNVNLINSTLTET 170
Db 1023 SNRYGYSNNTSSKLENIH-----ETENLSRRL--TDRIDLSKSG--MDENIOLKKE 1071

```

QY 171 AVORIKYNEKTEBALTSATETMLTKYQ--DSSHTDILDELTELTELAKSVTKNDVDFE 228
DB 1072 SFDSVSKYQVEKE-----LKVDLDDGDEAKINKLVKEIQYYKSRLEBAID----- 1118
QY 229 YLNTF-HDVMIGNNLFSG-----RSALKTASEL---IAKENLKTSSSEVGNVYN-PLI-- 275
DB 1119 YKRTIDNDIMQAKERGETITNELKNNIESKSEFLNDLYKRFGLTIESNEERSTPLIS 1178
QY 276 --VLTLQAKAFLLTTCRKLGLADIDYTPIMNEHLNKEKEFRVNIPLTISNTSPN 333
DB 1179 EGALSKIRBEIKTLIS-----NDENLOIKISEM-----DON 1210
QY 334 YKANGSDKDAKIIMEAKPGVALVGEISKDAIVLKVYQAKLKNYQIDKDSLEIYVG 393
DB 1211 FE-----IIEOR-----SKDILEFEKELODKIKDCYGFINSQGEIKAG 1249
QY 394 DIDXL-----LCPDSEOMYTNKIAFPREYVITKIAFTKQANSRLRYETANFYDSSTD 448
DB 1250 VEENIKNHPDVCITKKNVTLIDDIYKENE-IHKRIDSLSIESFPDSIEKMLNDKVSQC 1308
QY 449 I-----DLNKKKIESE--AEFSMLNANDGVMPITGISEFTLPING-----FGLVVD8- 497
DB 1309 IDKINDFVLKYIELEERCNEGOLNENK-IDNKIKALDNLALSOYDLEKRYADYDEF 1367
QY 498 ---NSRLVTLT--CKSYLRETL-----LATDSLNETKLIVPNGFTSNIVE 539
DB 1368 SERLSYIATLSEEFKSNKEMIPELESQKMLKOLSEDLNVEKDVIRLKESEYHVS 1427
QY 540 NQNLGEMLEPWKANKKAYVDHTGCVNGTKVLYNHEDGESQFIDGKLKTEYVIOYI 599
DB 1428 HIKLEEDF-----FKDLK--IRGEELKYSLEN--FTASYNDKQ--MLEYDLSKN 1472
QY 600 VKGKAIIY-----LKDEKNGDYI--YEETNNLEDPQ--AVTKRFTTGDSSRV 644
DB 1473 LENKTELLOSFPDLBOAKDKDKENFYDLFTKESKKKQMOSEIALMETNITGKXDEFV 1532
QY 645 HLIPTSONGEAFGNGFIISIRPSEBELSPFLIKSDAWVSGQTMISGNSLINSNVNG 704
DB 1533 DFNKKQSIIDSWFLN-IKDVYKMOE-----KSYSTIBKR--INLALGIGISFEND 1581
QY 705 TFRQULSLESYSTYGMNPNVNGFGKVTIRNSREVVPEBSYLOPSSKYSSEKTTTNNTG 764
DB 1582 IFNVKIGLESFK-----DGF-----EIKAEIIF--SNLOAKKIEOSVHLDFKQIG 1626
QY 765 LVELSRASSRGVINF 780
DB 1627 ESMLKVLDELKPVDF 1642

RESULT 4

F82909
hypothetical protein U293 (!imported) - Ureaplasma urealyticum
C:Species: Ureaplasma urealyticum
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: F82909
R:Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Helner, C.R.; Chen, E.Y.; Casseil, G.H.
Submitted to GenBank, February 2000
A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min
A:Reference number: A82870
A:Accession: F82909
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-1447 <GUA>
A:Cross-references: UNIPARC:UPI00000CIC06; GB:AE002127; GB:AF222894; NID:96899268; PTDN:
A:Experimental source: setovar 3; Biovar 1
C:Genetics:
A:Gene: U293
A:Genetic code: SGC3

Query Match 5.2%; Score 206; DB 2; Length 1447;
Best Local Similarity 20.9%; Pred. No. 0.092;
Matches 184; Conservative 141; Mismatches 306; Indels 248; Gaps 49;

QY 29 IKDIM-----NMIFKNTG-----GDLTIDEI-----LKN--QOLNEISGLDGVNS 70
DB 124 VQDVWNNDDHNNHLMKMTKTSFISHKLSDLLIKIQVLTPOKHEYOQLVNNLNGIDPKR-V 182
QY 71 LNDLLAOGNLTLSKEILKIANEON-----KVIN--DVNTK-----LDANIMLMNTY 116
DB 183 VQNLIVEGPAKIIDHQOLK--NSQNFGLIQKVINIDVMIKQOLKOLLSAITQIDIN-- 238
QY 117 LFKISMLSDVKNVYALGLOEYLSKOLKISDGLVYN-----NYLINSTLTE 167
DB 239 --LKATSTYTIINSYLWPEIKNLTER-----DRNLINIPDKLIKQIPLNLYQNVLD 290
QY 168 ITPAYORIKYVNEKEFALTSATETMLKTKODSHTDIDELTELTELAKSVTKNDVDFE 227
DB 291 -----QSDVFLKVNIEALINHQPLKQTTWNPDPINQVND-LSALSNLEIFETNETTNE 344
QY 228 FYLNTFHDVMIGN-----NLPSRSALKTASELIAKENLKTSSSEVGNVYNPLIV 276
DB 345 W--NQLITILINHAPIDKIEIIRNITSNSIINNKAQ--KQDIK--KQIDKIY--LLI 394
QY 277 LTLAQAKAFLLTTCRKLGLADIDYTPIMNEHLN-----EKEFRVNIPLTISNTPS 330
DB 395 KKVLOQYQ--TLNKSHTSVVKI-----NETIKTLIDSLFANQEIKTLSNTLSNMF 445
QY 331 NPNEYKAGSDKDAKIIMEAKPGVALVGEFISKDSI-AVLKY----- 372
DB 446 SNNLAKILNVEDQNSL-IRP--VAFIISNDLKTLIKTITNPSFILHASELANTPSF 501
QY 373 -----QAKLKNYQ-----IDKDSLEIYVGDIDKLCPDQS--EGMYTNKIA 414
DB 502 BELIVKLISFPQYTNLSNMLNFIQKILQNDKIDELLAAVIFKQISPOKQVQIQIINK-- 559
QY 415 FPNEVITKIAFTKGLN-----SLRYEVANPDDSGDIDANKKIESSEAEFSMLNA 468
DB 560 --DKVVT--FIKKLGNLTFRFDLYNKLNLNLPSSITNOQNTLK-----LLSE 602
QY 469 NNDGVMPITGISEFTLPINGFGLV-----VDENSLRVTLCKSYLRETLATLDSN 521
DB 603 QODSVINIKITIPD-FSPKQIISLIDVLKNETITSNDYIEVI--KSLDE----- 650
QY 522 KETKLIYPNGFISNIYENGUL-----EGENLEPWKANKKAYVDHTGCVNGTKVLY 573
DB 651 -----IDNHFQAVNNSVPLNKHENDSKDINKYIYV-----KTLF 695
QY 574 VHEGEPFQFIDGKLKTEYVIOYIK--GKAIIYLKDEKNGDYIYEETNNLEDPQAV 631
DB 696 AHEMDSTK--EKLKTIIDELTKKIVENNKKGLLYLNGCIGERT--SNLIINTPFG 749
QY 632 TKRFTTGDSRVHLIFTSONGEE-----AFGNFTI-----SEIRPSEBELSPBLIK 679
DB 750 TN--LKQNYKTLVQKVFQNLNLFBOVONLITVAINSLIDHKNYONCKTPEGELLTYINK 807
QY 680 SDAWVSGQ-----GTWISGNSL--NINSNVGTFRQULSLESYSTYSMNPNVNGFGKVT 731
DB 808 NQTOQIDKLKAKINKIISGSSSLIDELISTSPANTIKYFKLENLTVEDIN-KLSFNFV 866
QY 732 IRNSREVVPEBSYLOPSSKYSF--KFTTTNNTGVLV 767
DB 867 IKNI-----FMLEVNDGLVYLITLSSNAIKI 894

RESULT 5

T28679
fibrinogen-binding protein homolog - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T28679
R:Josefsson, E.; McCrea, K.; Ni Eidhin, D.; O'Connell, D.; Cox, J.; Hook, M.; Foerster, T
Microbiology 144, 3387-3395, 1998
A:Title: Three new members of the serine-aspartate repeat protein multigene family of S
A:Reference number: Z20510; MUID:99098700; PMID:9884231
A:Accession: T28679
A:Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA
A;Residues: 1-1315 <OS>
A;Cross-references: UNIPROT:O86488; UNIPARC:UPI0000052285; EMBL:AJ005646; NID:e1318791;
C;Genetics:
A;Gene: stdD

Query Match 5.1%; Score 203.5; DB 2; Length 1315;
Best Local Similarity 21.3%; Pred. No. 0.11;
Matches 178; Conservative 118; Mismatches 305; Indels 235; Gaps 45;

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QY 40 NTGSDLLDELKNOQLNEISGLDGVNSLNDLLAQNLDELSEIKI--ANONK 97
DB 139 STMEDLNTKQITISNOELQP-----DLOENKSVNAVQPTNEEK 177
QY 98 VLN-----DVNTKLDAL-----NLAINT-----YLPKITSLSDVMKQNALG 135
DB 178 KVDAKTESTLNTAKSDAIKSNDELTVNNSNNENNADIIIPRSTA-----PRIN 229
QY 136 LQIEYLSKQLEISDKLDVINNVLI--NSTLT-----EITPAYQRIKYNEKEAL 185
DB 230 TRKRIAVQSPSTEAK-----NVNDLITSNTLTVADAKNNKIYPA-----QDYISL 277
QY 186 TSAETNTLTKRKQSDSH-----DILDEL--ELTELAKSVTKNDV 223
DB 278 KSQITVDKVSQSDYFIKTSIVQVYGLNPEDIKIDIKDPNNGETIATAKHDYANL 337
QY 224 DGEFF--YLNTFHDVMTGNLFGRSALKTASELAKENLKTSGSEGVNVPFLIVLALQ 281
DB 338 IITYFTDYVDRFNQVGINV---SIMGADTIIVSGNDVEFNITIGT----- 383
QY 282 AKAFLLITTCRKILGLADIDYTPIMEHLNKEKEEFVNILPYSNTPS--NPEYK-- 336
DB 384 ----TYKTT-----ANIQYP-----DYVNEKNSIGSAFETVSHVGNENPEGYQTI 428
QY 337 ----ARSDDAKTIIMEA--KRGVALVGFELISKDSIAVLKYQA----KLHNQYIDDSL 387
DB 429 YVNPSENSTNAKLVAVHSSYPNNIGQINKD--VTICKIYQVPGKTYLTKGVDNNKEL 487
QY 388 SEIYVGDIDKLLCPDQEQMYTNNKIAPN--EYVI---TKIAFTKSLRKYEVANF 441
DB 488 TDVTNQYLQKITVGDNNNAV-----IDFGNADSAVVMWNTKPYTNSBPFLVQMTL-- 541
QY 442 YDSSTGDIANKKKIISSEAFPSMLNANDGVMPICITSETFL--TPINGFGLVVDNS 499
DB 542 --SSTGN-----KSVSTGNA--LGFTNNGSGAGQEVYKIGNYVEDTNKKGVDELGKGV 593
QY 500 RLVTLLCKSYLRETLATDLSNKEKTLIVP--PNGPISNIYVNGNL--EGENLEPMKANK 556
DB 594 GNVTVTVFDDNNNTKGEAVTKEDGSYLLIPULPENG--DYRVEFSNLKGYEVTPSKGN-- 650
QY 557 NAVVDHTGVNGTKVLVYHEDGFSQFIQDKLKLKTEYVIQYIKGKAAYLKDQKAGDY 616
DB 651 NBEIDNSG---LSSVILVNGKDNLSADL-----YKKRYNNGDY 687
QY 617 IYBETNN---ELBDFOAVTKRFTITGDSR--VHLIFTSQNGEBAF---GNFIISEIR 667
DB 688 VMEITNKGQIQDDDEKGISGVTVLTKDENGVLKTVTTDADGKXKFFDLNNGYKVFETT 747
QY 668 PSEELISPELIKSDAWVGSQGTWISGNSLINSNVNTPFRONLSLES--YSTSMNF--- 722
DB 748 P--EGYPTTVTSQSDIEK---DSNGLTTTGVINA--DNMTLDGCFYKTPKRYNNGY 798
QY 723 ---NVNNGFGK-----VTIRNSRVRVPSRYLOFSSKYSIKSFYTTTNT 763
DB 799 VMEDTNKGQDSTDEKGISGVTVLTKNENGVLTOTTTDQGX---QFTGLENGT 851
```

RESULT 6
T28677
rhoptry protein - Plasmodium yoelii
C;Species: Plasmodium yoelii
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T28677; C45521

R;Keen, J.; Sinha, K.; Brown, K.; Holder, A.
Mol. Biochem. Parasitol. 65, 171-177, 1994
A;Title: A gene coding for a high molecular mass rhoptry protein of Plasmodium yoelii.
A;Reference number: 220508; MWID:95021522; PMID:7935623
A;Accession: T28677
A;Status: preliminary; translated from GB/EMBL/DBD
A;Molecule type: DNA
A;Residues: 1-2269 <KE2>
A;Cross-references: UNIPROT:Q26223; UNIPARC:UPI000080871; EMBL:L27838; NID:g457145; PI
Mol. Biochem. Parasitol. 42, 241-246, 1990
A;Title: Identification of the gene for a Plasmodium yoelii rhoptry protein. Multiple c
A;Accession: C45521
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 2131-2269 <KE2>
A;Cross-references: UNIPARC:UPI000017B646; GB:M34283

Query Match 5.0%; Score 201; DB 2; Length 2269;
Best Local Similarity 21.6%; Pred. No. 0.29;
Matches 179; Conservative 138; Mismatches 285; Indels 226; Gaps 47;

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QY 34 NMIFKTNNGSDLLDELKNOQLNEISGL-----DGVNSLNDLLAQNLDELSEIK 87
DB 21 SMIKLNSG-----ILRKYTISNOIKNDLVSTYPEGREGFTSSL-----ELAKS 65
QY 88 ILKIANQNKVLNDVNTKDAINMLNNTVLPKITSMLSDVMKQNYALQIEYLSKQLE 147
DB 66 WEKTKLETTTELKSNSEYTRLEKEIRELFK---YLDEAEKYLEGLKLE--LKKIKD 121
QY 148 ISDKLDVINNVLI-----NSTLTET--PAYQRIKYNEKEALTSATETNLTKOD 198
DB 122 IIAKIEVKNVTVELKKEIKGNNAVYIDELANQSYKVTGYENK-----NTVNTISYFD 176
QY 199 SSHTDILDELTELAKSTKNDVDFEYVNTFHDVMTGNLFGRSALKTASELIAKE 258
DB 177 QIIEGID--TFYNEISYIKEDPIDIE-----DKTKLENI--RSKIDNVYDKIQKM 225
QY 259 NLKTSQSEGVN--YNFLIVLTAQAKAFLTLTCRKLLGLADIDYTPIMEHLNKEKEEF 317
DB 226 EIEYVSHLNNIETNNKLPFTLIEIKIT-----YBISKE--LNMKLEDF 269
QY 318 RVNILPPLSNTFNPYERKAGSDKDAI--IMEAKRGVALVGFELISKDSIAVLKYQAKL 376
DB 270 K--NKEKLSMKIS--DYDKKREQLSEYKSMLEIRHYN-----SQYVNDNKEBA-- 318
QY 377 KENYQIDKDSLEIVG--DIDKLLCPDQEQMYTNNKIAPFPEYVITKIAFTKLSLR 434
DB 319 KQNYVDSNEMETIIPNEDEISKIIEVKTMKDEILSKV---NTY---IDFNKK----- 366
QY 435 YEVYANPYDSSTDI-----DLNKKKISSEAF-----SMLNANDGV---YMPIGTIS 481
DB 367 YKETVNSHESQFTELVDKIAEVSDEKLCESFNDNKSILNETKNSIKETQONITLK 426
QY 482 ETELTPIINGGLVVDNSRLVTLTKCSYLRETLATDLSNKEKTLIVPNGPISNIYENG 541
DB 427 K-----VDEYIKV-----CKS--TWESI--TKFSKQTLMDMLNQNIKTYEYN 467
QY 542 NLEGNLEPW-----KANNKAAYVDHTG-----GVNGTKVL 572
DB 468 SIDKSYIEKEQQLTGKQTLKENKTFEFSLNHEANR--NELIKYFSDLKANLGINBEML 526
QY 573 Y--VHEDGFQFIDKLLKTEYVIQYIKGKAAYLKDQKAGDYIYBETNNEL----- 625
DB 527 YNQFTEKEKTFNDIKENKIHINEE--ISKIEIKIHASTY-----NISSETREIGINT 577
QY 626 ----EDFOAVTKRFTITGDSR--VHLIFTSQNGEBAFGNFIISEIRSEELSPEL 677
DB 578 ESLNTKVFKEV--KENVTNLIKIKELKHVDF--SDFGEE--GN-----IKYTOKI--KK 624
QY 678 IKSDAVVGSGGTWISGNSLINSNVNTPFRONLSLSY-----YSTSMNF 722
```

Db 625 INDDIMAVSQ-----QIDHINGLDDIQKSSSYSEMEQINKEVSNTEISND 675
Qy 723 NVNGFGK-----VTIRNSREVVERSYLOPSSKYISEKFTTTNTNGL 765
Db 676 NVBGIGKKQOIIVTKIDKKNIYB-----INKLSEISIKIEKDNISL 718
RESULT 7
118501
hypothetical protein C0760c - malaria parasite (Plasmodium falciparum)
C.Species: Plasmodium falciparum
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C.Accession: T18501
R.Lawson, D.; Bowman, S.; Barrett, B.
submitted to the EMBL Data Library, August 1997
A.Reference number: Z18935
A.Accession: T18501
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: DNA
A.Residues: 1-3394 <LAN>
A.Cross-references: UNIPROT:077384; UNIPARC:UP100008066; EMBL:Z98551; NID:e1331903; PI
C.Genetic8:
A:Map position: 3
A:Note: C0760c
Query Match 5.0%; Score 199; DB 2; Length 3394;
Best Local Similarity 20.6%; Pred. No. 0.61;
Matches 174; Conservative 122; Mismatches 322; Indels 226; Gaps 38;
Qy 48 DEIL-----KNQULNEISGKLDGVNGSLNDLIAQGNLDTLSKEILKIANEQKVLNDVY 103
Db 1201 DKILLLTKYEQLEENYKIKKKEEYLAH---CISELENNIERVYNEKILIDEQIN 1257
Qy 104 TKLDALNMLNTYLPKITSMLSDWKONVALGLOIEYLSKQLEISDKL---DIVINAVL 160
Db 1258 EKEKINININIKYL-ILEKEYEYONKNIINAQLENEKEKKQIQOEILIQKDMINVK-- 1314
Qy 161 INSTLTETPAYORIK-----YNEKEFALTSATETNLTKQDSHTDIL 205
Db 1315 LNEKNCDDIIKIYKEXKQYVHTLLOENKOSHVLKQKEVNL-----LNLNEKALKYHDHSL 1369
Qy 206 DELTELTELAKSVTKNDVDFEFYVNTFHDVMIANNLFGSALKTASSELIAKENLKTSGS 265
Db 1370 NKINILMLEEKENNKK-----NTFHL-----MNNL-----RVENNNLLKKMK 1405
Qy 266 EVGNVYVNLIVTLAQAFLTLTCRLKLGADLDYT-----PIMNEHLNKKESF--- 317
Db 1406 ELQNKYNTIIKKELNERIKQINVRNNVSTLSLRDKRSTGSIHQINNNMYNNNTHLGFNGA 1465
Qy 318 -RVNILLPTLSNT-FSNPNYKARGSDKDAKIMEAKPGVALVGFESKDSIAVLKVQA- 374
Db 1466 SKIN--NNISNLYSNMIMHSIRGSIIRKKEAEGNSIOARKNNKOSTDNI--INNTHNTD 1522
Qy 375 KLKHYQIQDKSLSEIVYGDIDKLLCPDQSEQMYT---NKIAPNEVYITKIAFTYKL 430
Db 1523 NINNMMNNNNNTNINSI-----NSNHLVYPPPPHNNVNSPKVGMCDVTLASGV 1570
Qy 431 NS-----LRYEVYAN-----FY 442
Db 1571 NKQDFFLINLENNENSPLEYEIRIKSLQEBLCDESEILKIKGKNILITCIETWKQFC 1630
Qy 443 DSSTGDI-----DLNKKIIESEAEFSMLANNNDGYMPLIGTSETFLTPINGFGLVVEN 498
Db 1631 KNSKEISRLKEICEQGEKFK-FFLLINKSN-----EKLKYN--SLICBEK 1676
Qy 499 SR--LVTLTCKSYLEETL--LATDLSNK--ETKLIVPPNGFL---SNIVENGNGENJLE 549
Db 1677 DKYDILVVDIKNNMENEIDKLNDINEKSYEIKLLKHENNNLINEMNLIKKNKSTENNIK 1736
Qy 550 PW-----KANNNGAVVD-----HTGGVNGKXVLY-----VHEDGESQFTGKTL 588
Db 1737 QKEBDYIKLKIKKDKTNIQNEYNDLLEKNEVVVKNMMLYNDMMVLLKEHKEEILFLIKENI 1796

Qy 589 KLKTEYVIQYIVKGAAYLKDEKNQDGYIEEFTN---NELDEFOAVTKRFFITGDSRYH 645
Db 1797 K-----ILQ-----KNTYLANDMFKQNIYVNDNNLLKRLDQLFNIDQLKHLDTNQH 1846
Qy 646 LIFTSQNGEAFAGNFIISEIRPSEELLSPELIKSDAVY-----GSGGTWI 691
Db 1847 L-----EQLKVDYL--EIKERLKIEKTKINKQEKYIIQIQKDNLLNDFNSTTTT 1896
Qy 692 SGNSLINNSNVNGTRQNLISLSESYSTSMNFVNGFGKVTIRNSREVVERSYLOPSSKY 751
Db 1897 NNNNNNDNNNDNNNDNNNDNTYQQFIHSLKAN-----LNSRLLEKLSLNEKIQTL 1950
Qy 752 ISEK 755
Db 1951 SDEK 1954
RESULT 8
555805
alpha-toxin - Clostridium novyi (ATCC 19402)
C.Species: Clostridium novyi
A.Variety: ATCC 19402
C.Date: 28-Oct-1996 #sequence_revision 08-Nov-1996 #text_change 09-Jul-2004
C.Accession: S55805; S71294; S71158; S44273; I40834; S44272
R.Hofmann, F.; Herrmann, A.; Habermann, E.; von Bichel-Streiber, C.
Mol. Gen. Genet. 247, 670-679, 1995
A.Title: Sequencing and analysis of the gene encoding the alpha-toxin of Clostridium n
A.Reference number: I40834; MUID:95342160; PMID:7616958
A.Accession: S55805
A.Status: nucleic acid sequence not shown
A.Molecule type: DNA
A.Residues: 1-2178 <HOF>
A.Cross-references: UNIPROT:046149; UNIPARC:UP1000017CA46; EMBL:Z48636; NID:g728537; P
A.Molecule type: protein
A.Residues: 1-15 <HOW>
A.Cross-references: UNIPARC:UP1000017CA47
R.Hofmann, F.
submitted to the EMBL Data Library, March 1995
A.Reference number: S71158
A.Accession: S71158
A.Molecule type: DNA
A.Residues: 1-1179, 'LKV', 1183, 'LVTHIGE', 1191-2178 <HOS>
A.Cross-references: UNIPARC:UP10000BBABE; EMBL:Z48636; NID:g728537; PIDN:CAA88565.1; I
R.Hofmann, F.; Habermann, E.; von Bichel-Streiber, C.
submitted to the EMBL Data Library, July 1993
A.Description: Sequence analysis of Clostridium novyi alpha-toxin: a member of the fam
A.Reference number: S44272
A.Accession: S44272
A.Molecule type: DNA
A.Residues: 1-243; I204-2178 <HQA>
A.Cross-references: UNIPARC:UP1000016EB32; UNIPARC:UP1000016EB33; EMBL:Z23281
C.Genetic8:
A:Gene: tcn-alpha
C:Keywords: virulence factor
F:1880-1899/Domain: cpl repeat homology <CP12>
Query Match 4.9%; Score 194.5; DB 2; Length 2178;
Best Local Similarity 20.1%; Pred. No. 0.54;
Matches 187; Conservative 126; Mismatches 296; Indels 323; Gaps 46;
Qy 7 LSVLALPSFIDYFNGIYGFATGIDIMMIFKNTMGDDTLDELKQQLNLEISGK--- 63
Db 25 LILDLLENFNRDIBG-----TSVEIYSKLSK-----LNLVDNYQTYRPSSGRILA 71
Qy 64 ----LDGVNGSLNDLIAQGNLDTLSKEI-----LRIANEQNKVLDVNTYKL 106
Db 72 LENRDSIYSRLRLINKSRSTSLASKVLSFIWIGFPISDQSLSYNNMKKFNKDYNIRL 131
Qy 107 --DAINMLNTYLPKI-----TSMLSDVKNKONVALGLOIEYL 141
Db 132 FYDKNSILVNTLTKALTAIIQESSKVIIEQNQSNILDGYGHNKFYSDRMKLIVRYRGRELMKL 191

142 SKOLKEISDKLVINNVNLINSLTEITPAYORIKYVNEKEALTSATETNLTKTODSSH 201
YENKKQ--NSVDYDIIINFLSNYFKYDICKLNCKNNNNKMIAT--GATDIN----- 240
202 TDILDELTE--LTSLASVTKNDVDGFEFYANTFHDWIGNLFGRALAKTASLLAKEN 259
241 -----TENILNKLKLS-----YY--YQELQTN-----LAAASILRIAI 274
260 LKTSGEVGVNYYNVLIVLALQAKAFLLTTCRKLGLADIIDYTPIMNHELNKEKEFRV 319
275 LK-----KYGCVY-----CQDLFLPGVN----- 292
320 NILEPLNTSNTSNPNYERKARGSDK--DAKIMEAKPGYALVGFELISKDSIALVKYQAKL 376
293 ---LSLENDISKPN-----GMDSNYMEALIF-----EALIA-----NEKKL 324
377 KHNK-----QIDKDSLSEIYVGDIDKLCP-----DOSEQWY-----YTNNKAF 415
325 MANNPYRYMEQVSEIERILISFVRNHDINDLILPLGDIKISQLEILSLRKAATGKKTFF 384
416 PNEVYIT--KIAFTKLNSL--RYEVLANF-----YDSSTGDI DLNKKIESS 460
385 SNAFLINNSLNLINLSQLENNYELINSLIOEKFKICEYDYSYINSV--SELVLETP 442
461 AEFMLANNDGVYMP--IGTISETFPLPING-----FGLVV 495
443 KNLSM--DGSSEFYQOIIIGYLSGFKPEVNSTVFSPGNIYSSATCDTYHFKNTPMLG 499
496 DENSRVLTLNCKSLARE-----LLATDLSNKE--TKLIVPNPGFISNVEKNLEGE 546
500 SONEIETBASNNLTFSTKHDEFKSSWILRSNIAKEOKLTKTYIGRTLANE---DGL 554
547 NLEBPKANNKAAVYDHTGCVNGTKVLYVHEDEFSQFIDGDKLKT-----EYV 595
555 NFNKKQVLTSELLKVLBEVNSTKIYENYDMLMLQIQGDDISYESAVNVPGRKPKNSIL 614
596 IQYIVKGAALYYLKOENKGDYIYAEVTNNELEDFOAVTKRPTTGDSRVHLIFTSQV--G 653
615 IOGVDDPANYFYF--ENGIVQSDNINNIIISRFNDIKIKLT-----LIGHGVN 663
654 EBAFGNFI-----ISEIRPS--EELISPELTKSDAMVSGQWISGNSLNTN----- 699
664 PKLFGKTVNDLYNIIKPKLQHLERE-----GYLKNKKYKLNIIIGCYWFTP 712
700 -SNVNGTF-----RQNTLSBSYSTYSNMFVNGFKVYIIRNSREVEREYSLQPSK 750
713 KVDINSTFVGKLFNKISRDLQPKGFSKNQLEISAN--KKAIRINRE--GKREVLDFYFK 767
751 YISEKFTTTNNNGLYVELSRASRGVINF 782
768 WVS-----NTDLIAE--QISNKYVYVWNE 789

RESULT 9
C97033
uncharacterized protein, probably surface-located [imported] - Clostridium acetobutylicum
C/Species: Clostridium acetobutylicum
C/Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C/Accession: C97033
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Benmect, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld
A/Reference number: A96900; MUID:21359325; PMID:21359325
A/Accession: C97033
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1227 <R>
A/Cross-references: UNIPROT:Q97K41; UNIPARC:UPI0000CA0A1; GB:AE01437; PIDN:AAK79054.1;
A/Experimental source: Clostridium acetobutylicum ATCC824
C/Genetics:
A/Gene: CAC1080

Query Match 4.9%; Score 194; DB 2; Length 1227;
Best Local Similarity 19.6%; Pred. No. 0.26;
Matches 173; Conservative 146; Mismatches 320; Indels 242; Gaps 45;
9 VKALPSFIDVFNIGYATGATGKIDIMMIFKTNVGGD--LTLDLKLKQ--QLNEISGKL 64
416 VKEVKTLIDFYNHAAACQTLTLDYKNDVPAHQVQDDVALTSMLKTRDCKTLKALODKI 475
65 DGVNSLNDLAAQ--GNLD-----TE-----LSKEIILKANEQNK-----VLNDV 102
476 DSIINSLKINSGINIGDYSKQATEAVDASKLEAVNDLKKIKADGRDLTIOEIRDSV 535
103 NTKDALINMLANTYLPKITSMLSDVMKQNTALG-----LQIEVLSKOLKEISDKLDVIN 156
536 KTIIDYINSTN--VSKGDSVSDYI-----TIGIDGTEINIEFVNERIKESGITTIEN 589
157 VNVLINSLTLREIPAYORI--KYNEKEFALTSATEN-----LTKQDSSHTDI 204
590 IKVVI--EPVQLEEVYRIYGVGVVDYKTLGINNVDNNIIYINAEIKKDKDVKI QDI 648
205 ---LDELTELTELAKSVTKNDV--DGFEE-----YANTFHDWIGNMLFGSA 247
649 QTRVDNTINNIDVINKIAGDAVLSDFENIGITDYODIIDYVNA--DLKIQN----- 699
248 LKTASLILAKENLKTSGSEGVNYYNVLIVLALQAKAFLLTTCRKLGLADIIDYPIYN 307
700 YKQVDDIIEHVEAKISS-----YEALMRINIGEA-----VTDDPKALGLTDIN----- 742
308 EHLNKEKEEERVNIILPILSTPSNPNYERKARGSDKAKIIMEAKPGYALVGFELISKDSIA 367
743 -----DGLLVATDILNKNYKTKAD-----EVLARVQA 770
368 VLKYOAKLKAHNYQIDKDSLSEIYVGDIDGLCPDQSEQ--MYTNKIAFPENEYITKIAF 426
771 QIEIYRLAMQIN-----LGKATADYNTLGIIDVNDLSILTYVMDLQGRNV----- 817
427 TKKLNSLRYEVYANF-----YDSSTGDI DLNKKIESS--EAEFSLMANNDGVY 475
818 --NVDEVKAEIERKNIQIYNALLKIDSGSATID--DYRTIGITVYIDVNIISYVIRIKQMI 874
476 PIGISTEFTLPINGFGLVYDENSRLVTLTKSYIAKETLLATLQSLNKEKTLIYPPNPFIS 535
875 PVSVDARFPIITILN--NMIVSVSGTIT-----DSATGTPLOGEVIERFRGEN--- 921
536 NIYENGNLLEGENLEPMKANNKAAVYDHTGCVN-----GTRKLYVHEDEFSQ--FIGDKL 588
922 NIA--GNYFSKNSPVEAT-----VDAQKYSIQLEPGSYTVAIKKDGVTQNFVITSNG 974
589 KAKT-----EYVIOYVK-----GKAALYL--KDEKNGDYIEETNNELED 627
975 KAKTVLQNIQLVNLQYTVSGVVDQAQTGNPLQGVAIRFRIGQNKSGDY--YSVNGEVVV 1033
628 FOAVTKRFTGTSS-----RVMLIFTSQNGEAPFGNFIISIRSEBELSP 675
1034 YTDAQGYTVSLDGYTAAKKGDTYNVSVVISEATNNTQNTVTSQTL--SENOYRV 1092
676 ELIKSDAMVSGQWISGNSLINSVNGGFRONLSLESY-----STYSNMFVN 725
1093 VL-----TW--GANLDDLDSHFSGTGSGQGINVYQQAQPSAQVGVTVVSLDIDAK 1140
726 -GFGKVTIRNSREVEREYSLQPSKYSIKSEFTTTTNNNGL 765
1141 FGVPETV--TVVDKSGSYTVSPDFSGSSASAKSL 1178

RESULT 10
G82887
hypothetical protein ut474 [imported] - Ureaplasma urealyticum
C/Species: Ureaplasma urealyticum
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C/Accession: G82887
R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Casseall, G.H.
submitted to Genbank, February 2000

[illegible]

Db 899 PNRKY-TFEKVLIOER-----NNLNMYDLNKK-----INLTD 930

RESULT 11

G82934

hypothetical protein UU094 [imported] - Ureaplasma urealyticum

C:Species: Ureaplasma urealyticum

C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000

C:Accession: G82934

R:Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Caswell, G.H.

A:Submitted to GenBank, February 2000

A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a ma

A:Reference number: A82870

A:Accession: G82934

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1054 <GLA>

A:Cross-references: UNIPARC:UPI00000CIB96; GB:AE002109; GB:AF222894; NID:96899045; PIDN

A:Experimental source: serovar 3; biovar 1

C:Genetics:

A:Gene: UU094

A:Genetic code: SGC3

Query Match 4.7%; Score 189.5; DB 2; length 1054;

Best Local Similarity 21.3%; Pred. No. 0.34;

Matches 174; Conservative 127; Mismatches 292; Indels 225; Gaps 40;

18 YP----N0YGPAGCIDYMMYFKTNTGDL-TLDELTK-----QQLNBI----- 60

332 YFGANSNKEFRGTHSYTLNNEITQASYEODIFSDHKIKNELKKNEQQILKEVAF 391

61 SG---KLDGVNSINDLLAQNLDLTLSKEILK-IANBQNVLDVNTKLDALNLMN-T 115

392 SGYVDAIDISISIR-----LKGVDANLNLKEFLQSSQDFRNLTYNIT 436

116 YLPKITSMLDVMKONVALGLQIEYLSKOLKEI--SDKLDVINVNLINSTLTETPAY 172

437 QONNLTNLIT-LITNSNGLVIDGFKRLKEI-LYNNPSIDQ-SVKQNTYISKIDSMOPKN 494

173 QRIKVAKEFALTSARETNLKTQDSSHDYIDELTELTELASVTKND-----VDG- 225

495 NLIABIGQIRTLTLDISISLTKT-----YKEIINKLELISLIEARSKOPKNGYFIDGL 549

226 ---PEFYLTADHWIGNGLFGRSALKTASLILKENLKTSGSEGVNVNPLYLTLLQA 282

550 DELSFPLN-----LK-QNDLPSINFKI-GDQNTLYLD----- 582

283 KAPLTLYTCRLGLADIIDYTPINNEHLNKEKEF-----RVNILLPLS-NTFSNPNY 334

583 ---LIEVKKIAN---NLIPHENQYDPKQOIISTNYPLTKIKLIDLSLNKNDQLDY 633

335 EKANGSDKAKIIMEAKRGALVGFETSKOSIA---VLKYQAKLKNTOIDKSLSEI 390

634 HK-----GVEMIFSLKKQOIAPEFYIKYIDELLQNTMKNKENTKL 677

391 VYGDIDLKLCPOSEQMYTNKIAFPNEVYITKIAF-----KCLN-SLRYE 436

678 ---LDMILLPKITSNDPSINDLSKYPKYGISKPEITSKELEYDONNLLIKQLIKYRYK 733

437 VTANFYDSTGDIIDLNKKLES-----SEAFSMLNANDGVMPIGTISETF 484

734 VLVAAEPDIRPLPLLPQKPLSFIDGLGMEQIKKEPPYKIVLAKNDVYDHTISISQPOE 793

485 LTPINGGLVVDENSRLVTLTCKSYLRETLIANDLSNKE-----TKLIYPPNG 532

794 LT-----TLIFQDRSDHDKYKIGYVFPYPTHVTQTHMPS 827

533 FINSIVENGMLLEGENTLEPPKANNKNAVVDH-TGSVNGTQKLYLVHEDSEFSQFGDKLK 591

828 -MKAILIENISLRNDRLP-----NKKYVQQLMWLFYKKWVFNPPLAIYETFBGDK-KIP 879

592 TEVYIQYIVGKKAIVLKDEKNDYI-----YEETNNLEDPQAVTKAFITGDSRVLHI 647

Db 880 NDQKVKLLIDONLKNKYKNDKSDNTYCEGPDFKHFSSNLEN--KVGNQTIENLILAKIKTI 937
Qy 648 FTSNGE-----AFGNFIISSEIRSEELSPLEI-----KSNAMWGSQGTWISGN 694
Db 938 KT--DGGELVQDLAGRKTIATSAVDQJNLTQLIDYKLLFGKQVLD---KQDVLSAV 992
Qy 695 SLNINSVNGTFRONLSLESYSTYSNPNVNGFGKVTI 732
Db 993 AFRNGLTNDSDQTNV---LNNDEIKYNINILKKVVI 1027

RESULT 12

T30822
Impl1 protein - Mycoplasma hominis
C/Species: Mycoplasma hominis
C/Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C/Accession: T30822
R/Jensen, L.T.; Ladefoged, S.; Birkegaard, S.; Christiansen, G.
Infect. Immun. 63, 3336-3347, 1995
A/Title: Selection of Mycoplasma hominis PG21 deletion mutants by cultivation in the pre
A/Reference number: Z18884; MUID:95369882; PMID:7543881
A/Accession: T30822
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1365 <JEN>
A/Cross-references: UNIPROT:Q49525; UNIPARC:UP100000BC623; EMBL:U21962; NID:G790243; PIR
C/Genetic:
A/Genetic code: SGC3

Query Match 4.7%; Score 189.5; DB 2; Length 1365;
Best Local Similarity 18.5%; Pred. No. 0.48;
Matches 171; Conservative 137; Mismatches 317; Indels 299; Gaps 39;

Qy 1 MQQNKLSVYALPSFID-----YFNGIYGAIGIKDINNIFFKTT 41
Db 553 IKSNNTASMQSAKSLDAKVAIYTKLETENKDEAKFELKQTRNIOEFIN--TKRNP 611
Qy 42 GGDULTDELKNGQLNEIS-----GKLDGVNSINDLLAQGNLDTLSKEIILKINEO- 95
Db 612 NYSELLSQLTYSKDSKDSVTDSSNKSQDIESANTELKQALKAKADKQVQADNLASIKEQ 671
Qy 96 NKVLNDVNTKLDALINILANTYLPKITSMLSDVMKQNTAL-----GLQI--EYLSKQJKE 147
Db 672 NNSVSNANTISAKLTQDQNTIQAKTELEKEIQKANAISNTTASMQSAKSLDAKVAE 731
Qy 148 ISDKLDVIN-----VNLINSTLTETTPAY--ORIKYNEKEFEALTSATE 190
Db 732 ITKKLETFNKKDEAKFELKQTRNIOEFINT--NKNPNVSELLSQLTYSKDSKDSVTD 789
Qy 191 TNLTKQDSSHTIDIBELTELAKSV-----TKRD-----VDGFEFYNTFR----- 234
Db 790 SSNKSQDIESANTELKQALKNTAKAKSSIDNELRLPKDLQSKIEEFPRIINTPMSWISSK 849
Qy 235 -----DVMIGNNLFGRSALKTASELIAK---ENLKTSGSSEVGVN----- 270
Db 850 LETTKNKLABELTKRADIKNNPSSSKQALMDSQOVQKLGNEILKITTTFPGVETKSN 909
Qy 271 --YNFLIVTALQAKAF-----LTLTCKKLGLADIDYTPPINNEHLNK 312
Db 910 IGR--LFLTQAQAEQFNNSDVVDKLNKAMEKQTLSSKQKLGQSTKYDYLQJLSTEMST 966
Qy 313 EKEEFVNILPTLSNTPNEKARGSDAKIMEAKPGYALVGEISKDSIAVLAKVY 372
Db 967 QESTIKKIVNIQAHIRNNLNSQTRLEAD---KLIANMKRGYG-----DKVGIESLQAK 1017
Qy 373 QAKLKNNYQIDKDSLSE-----IYVGDIDKLCPCDSEQWYTYNK----- 412
Db 1018 QDLMDSDVLSVDLSKODFKALKRVLVGDVTK---NPPVSWFPIKRNNSIENYQJLRN 1073
Qy 413 --IAPNEVYITTKIAFTKGLNSLRVEYVIANFYDSSGTDIDLNKKKIESSEAPESMLNAN 470

Db 1074 LILVRENEILDK--AKDLK--RAEKTIKFDVENINSILDORAKRLQ-----EILNAXN 1124
Qy 471 DGVYMPIGTISERFLPPIINGFGLVVDENSLVTLTCKSYLRETLATDLSNKETKILVPP 530
Db 1125 D-----LSNFTL-----NHQKQFTAKDITPK----- 1146
Qy 531 NGFISNIVENGLEGNLEBPKANRNAAVVDHTGVNGTKVLVYHDEGFSQFIDKRLKL 590
Db 1147 ----ISLEN-----KLEINQY----- 1160
Qy 591 KTEYVIQYVKGAAAYLADKNGDYIYEFTNNELEDPOAVTKRPTITGDDSSVHLIFTS 630
Db 1161 ----LPIIKERAKVISE-----IEKKKELEDI--IRSNFYLM--EKVEI---- 1199
Qy 651 QNGEAFGCGNFIISSEIRSEELSPLEISDAVWGSQGTWISGNISNINSVNGTFRONL 710
Db 1200 -----NKYISELNKQVLEIRSNINPENKESIKDYL--DNINIKENVS--LKEVI 1246
Qy 711 SLESYSTYSNN--FVNGFGKV-----TIRNSREVPERSYLOPS-----SKYISE 754
Db 1247 INNSNQYSINRLSTVPEPIKVAQTRSNNLASLAEIQPKPFLDIDKNLKEVKKILDE 1306
Qy 755 KFTTTNNTG-----LYVELSR 771
Db 1307 NKTLSNDNIAKNEKIRLVDRSR 1330

RESULT 13

ORF MSV156 hypothetical protein - Melanoplus sanguinipes entomopoxvirus
C/Species: Melanoplus sanguinipes entomopoxvirus
C/Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
R/Afonso, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L.
J. Virol. 73, 533-552, 1999
A/Title: The genome of Melanoplus sanguinipes entomopoxvirus.
A/Reference number: Z20484; MUID:99102612; PMID:9847359
A/Accession: T28317
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1127 <AFPO-
A/Cross-references: UNIPROT:Q9YVT6; UNIPARC:UP100000F6900; EMBL:AF063866; NID:G4049647;
C/Genetic:
A/Note: MSV156

Query Match 4.7%; Score 189; DB 2; Length 1127;
Best Local Similarity 19.4%; Pred. No. 0.39;
Matches 161; Conservative 150; Mismatches 290; Indels 230; Gaps 38;

Qy 31 DINNMTFKTNVGGDLTL-DEILKN-----OQLNIESGKLDGVNSIND----- 73
Db 168 DIANKLKLVSSPEKDLIEQIYGNINKKEIFGNIDNVQKEINKQDELNKLDESKKE 227
Qy 74 LLAQGNLDTELK--EILKIAN-----EQNVLNDVNTKDALINL---MLNTYL 117
Db 228 IKQSEELNTIDKQBELIKKLDKEINFNIDEKQKLLQJNSKINTLENIGVNWVLYT 287
Qy 118 P---KTSMLSDVMKQNTALGLQIEYLSKQK--ISKLD--VINNVILNSTLTET 169
Db 288 ETKNKLSNQLNELNLDSTI-----KSLDEKQKLLBELDNINNTISLVKSSYTKIT 339
Qy 170 PAYORIKYVNEKEFEALTSATETNLAKTKQDSSHTIDILETELAKSVTKQNDVDFEFP 229
Db 340 NIOQLLE-----SLTDFNNANININELSKIKLPD--NDIQKLNNDITBQNNKLTDF 391
Qy 230 LNTFHDMVIGNNLFGSALKTASSELIAKENLKTSGSEVGAVNFFLIVTALQAKAFVLT 289
Db 392 NN-----STRIFKEKLDTEYKIKIDIKNNNLQKLEESYKKIDEGT 431
Qy 290 TCKKLGLADIDYTPIM--NEHLNKEKEFRV-----NILPTLSNTP 329
Db 432 EYTK--NKINKEYNDIIEILKNNNLQKLEENKKIDEGTEYVYKKNKINKEYNDIIEILKNNL 489

QY 330 SNPNTEKARGSDKAKIMEAPGYALVGFELSKDSIAVLKYYQ---AKLKNNY-QIDKD 385
DB 490 QRLBENKNNIDKLTAKLNDIESNTL-----FNKLNISDPKDSREIAKLTNEYQLRCD 545
QY 366 SLSEIVGDDIDKLCPPDSEOMYYNNKIAFPNEVITKIAFTKLANSLAEVTANFYDSS 445
DB 546 LLENTI-----NK-----TNE-LMKLS-DNKLSLE-----OLYDS- 573
QY 446 TGDIDILNKKIIESSAEFSEMLNANDGVYPIGTISEFTLPINGGLV-VDENSRLVTL 504
DB 574 -----KNIIDGIDIKYINSLAKKNDKI-----DEFTSNIEKFDIYNVENKFGML 619
QY 505 TCKSYLRETLATDLSNKKETKLIIVPNEGFSINIVENGNLEGENLEPWNKNNKAAVVDHTG 564
DB 620 -----DSIINKIINNOQFK-----EYINSKIDSKSNELSTWDDIIFNAGQJASITN 666
QY 565 GVNCKTKLVNHEDEGFSQPIGDKLKLKTEYVYQYVKGKAAI-YLCKEKNDDYIYEETN 622
DB 667 NIEN-----ISNKIKDLNEFIISNEDSSKELDEIRKYOQCFDKIKDAMN 711
QY 623 NELEDPQAVTKRFITGDSRVHLIFTSQNGEAFGNFIISIRPSEELSPELIKSDA 682
DB 712 TEVASFETLQKDIDISIKSN-----INELTNAYDIDITNKANDDD 751
QY 683 WVGSGTWISGNSLININSVNGTFRONLS-----LESYSTSMNFN-VNGFGKVT 731
DB 752 KLNNGYSBPK-NLYNNASDLDLDTIOKNDEKVKQLENEKKNKNSIIBINDIVNNFIEL 810
QY 732 IR-NSREVVFERSYIQFSSKYSIEKFTTTTNT---GLYVELSRASSKCVI 778
DB 811 IKFNNTS-----TNKSLNELLTVDINDIKIIFKLYKEIKLNKISTNLL 851

RESULT 14

Imp1 proteain - Mycoplasma hominis
C/Species: Mycoplasma hominis
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T18351
R.Jensen, L.T.; ladefoged, S.; Birkelund, S.; Christensen, G.
Infect. Immun. 63, 3336-3347, 1995
A>Title: Selection of Mycoplasma hominis P621 deletion mutants by cultivation in the pre
A/Reference number: Z18884; MUID:9536982; PMID:7543881
A/Accession: T18351
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1051 <JEN>
A/Cross-references: UNIPROT:Q49524; UNIPARC:UPI00000B95B; EMBL:U21961; NID:g790241; PID
A/Genetic code: SGC3
A/Genetic code: SGC3

Query Match 4.7%; Score 187.5; DB 2; Length 1051;
Best Local Similarity 18.6%; Pred. No. 0.41;
Matches 171; Conservative 135; Mismatches 316; Indels 289; Gaps 39;
QY 4 NNNKLSVKALSPID-----YNGIYCATGTCOKIDIMNMFKNMGCD 44
DB 242 NNTASMOAKSSLDKVAETKLETNKDKEAKFNEKQTRNOIQEPIN-TNNKNPNYS 300
QY 45 LTLDELILKNQOLLNEIS-----GKLDVNGSLINDLAQNDTELSKILKIANEQ-NKV 98
DB 301 ELISQLTSSKSDSVTSNKSQSDIESANTBELKQALAKANDPKVQADWLASIKEQLNNS 360
QY 99 LNDVTKLDAIINLMNTYLPKITSMLSDVMKQNTAL-----GLQI-EYLSKOLKEISD 150
DB 361 VSNANTISAKLTDKNTTIQAKTELEKEIQKANOAIKSNNTASMOAKSSLDKVAETK 420
QY 151 KLDVYIN-----VAVLINSTLTLEITPAV-QRIKYVNEKEFALTATETNL 193
DB 421 KLEFPNCKEAKFNEKQTRNOIQEPINT--NKNPNYSLEISQLTSSKSDSVTSN 478
QY 194 KTKODSSHTDILDELITBELTBLAKSV-----TKND-----VDGFEFYLTTFH----- 234

DB 479 KSDISANTELKQALNTAKAKSSIDNELRPLKNDLQSKIEBFGRIRNTNFSMISKLET 538
QY 225 -----DWNIGNNLREGSLAKTASBLIAF---ENLTKSSSEGVN-----Y 271
DB 539 TKNKLAEBITRADAIKNNPSSSKQALKDSOQVOQLGNELKTTIEBFGRKVKETKNSNIGY 598
QY 272 NFLIVLTLQAKAF-----LTLTCRKLGLADIDYPIPMHELNKKE 315
DB 599 R---LFLKAOEQLNNSVDKLIKAMERKQTLSSKQKLGNOSTQVLTQUSTEMSTDS 655
QY 316 EFRVNIPLPTSNFPNEYKARGSDKAKIMEAPGYALVGFELSKDSIAVLKYYQAK 375
DB 656 TIKKVTIVIQAHIRNNLSQYRLND---KLIANKRGYG-----DKVIGESLQKMDL 706
QY 376 LKANTYQIDKDSLSE-----IVGDDIKLACPPDSEOMYYNNK-----I 413
DB 707 MDDSVLSYDDSLKODFNKALRVLVGDYTK---NPPVSWFINKNRSIENYQNLRLNL 762
QY 414 AFPNEYVTIKIAFTKQNSLAEVTANFYDSTGDIIDNKKKIESSAEFSEMLNANDGV 473
DB 763 VRENELTDK---AKDLCK-PAEKTIKFVDENINSLDQRAKLO---ETLNKND-- 811
QY 474 YMPIGTISEFTLPINGGLVVDENSRLVLTCKSYLAEETLATDLSNKKETKLIIVPNGF 533
DB 812 -----LSNFTL-----NHQNGQFATDITPK----- 832
QY 534 ISNIVENGNLEGENLEPWNKNNKAAVVDHTGNGTKVLYVHEDGEFSQPIGDKLKATE 593
DB 833 -ISLEN-----KLANEINOY----- 846
QY 594 YVIOGYVKAALYLIKOKNDYIYEETNNELEDPQAVTKRFITGDSRVHLIFTSQNG 653
DB 847 -LPLTKEKAVSKISE-----IEKNNKELEDI--IRSNFYLM--EKVEI----- 885
QY 654 EEARFGNFIISIRPSEELSPELIKSDAVNGSGTWSGNSLININSVNGTFRONLSLE 713
DB 886 -----NKYIELNKKQVLELNSNINFEKMSISDITL---DNLNKENV-SLKEVIINN 935
QY 714 SYSTYSNM---FNVNGFGK---TIRNSREVVFERSYIQFS---SKYISEKFT 757
DB 936 SNAQYSNIRLISYTPBEFIKVAQTRSNRLSLAIIQFEPRLDIDIKLKEVKKILDEKKT 995
QY 758 TTTNNTG-----LYVELSR 771
DB 996 LNSDNIKLNKIRLVDRSR 1016

RESULT 15

conserved hypothetical U292 [imported] - Ureaplasma urealyticum
C/Species: Ureaplasma urealyticum
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C/Accession: B82909
R.Glass, J.I.; Lefkowitz, B.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Caswell, G.H.
submitted to GenBank, February 2000
A/Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a mi
A/Reference number: A82870
A/Accession: B82909
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1830 <GLA>
A/Cross-references: UNIPARC:UPI00000C1C05; GB:AE002127; GB:AF222894; NID:g6899268; PIDN
A/Experimental source: serovar 3; biovar 1
A/Genetic code: SGC3
A/Genetic code: SGC3

Query Match 4.7%; Score 187; DB 2; Length 1830;
Best Local Similarity 20.2%; Pred. No. 0.93;
Matches 173; Conservative 139; Mismatches 276; Indels 270; Gaps 43;
QY 20 NGIYFATGKIDIMNMIFKNTGTGDLTLDELTK---NQQLNLEISGLDG-VNGSLNDLL 75

Db 561 NNIGTONISKKILYDVFRRKIIINDQNLVELIKGFHSQLEFNENKSQIKSLIKALISDLV 620
Qy 76 AQGNL-----DTELSKEILKIANE--QNKVL-NDVTKLDAINMLNTYL 117
Db 621 SSHKLEIIRIIGEFATDNLKONNEFLKNLIIQNKLTQTKSLDNIINVFADLPDNDNEYL 680
Qy 118 PK--ITSMLESDVMKQNYA-IGLQIEYLSKQKEISDKLDVINAVLI-----161
Db 681 LQGPLSNVLAKIVTKNALLTRRIDNLFNDLFXDQTLLDA-TYNILIRVQGNIPDFIKT 739
Qy 162 ---NSTLEITPAQRIKYNE-KFEALTSATETNLTKQ---DSHTDIIDELTE---210
Db 740 PQAHLIKKILSKGTNKLINTLKLNTIDLLTDS--KYVAGIFDSSSETSIIINLIQKSIDF 797
Qy 211 ----LTELAKSVTKNDVGFEPFLNTFHDVMIGNNLFGRSALKTASELAKENLKT--S 263
Db 798 TSXSFISDVDDLTSNDV-----LNEM-----KEFIKTIILN 829
Qy 264 GSEVGNYVNFIV-----LTALQAKAFLTLTTCRKLIG-LADIDYTPIMNEHINKKEE 316
Db 830 SSTIKNIFNGIIVLVSNNTPLKTSFDFENVLLKNLJAVLEKDWI-----TNQTK 882
Qy 317 FRVNILPFLSNTFSNPNYEKARSGDKAKIMEAKPGYALVGFEISKOSIAVLKVQAKL 376
Db 883 LKSLIRMSVDLKNPOTONFVTSIED-----FYANKLGDVLISANNSLL 927
Qy 377 KHNVAIDKDSLEIVGDIDKLCPDQSEQVYTNKLIAPREYVITKIAFTKDLNLSLRYE 436
Db 928 KSN-----MSDIWDLI-----KEVVDLHSSSEYDLIFS 957
Qy 437 VTANF-----YDSTGDIDL-----NKKKIESSEAEPSMLANNQGVMPIGTISE 482
Db 958 IINDFIHPQNYDLNINIDLLPLIKSTNKELODKVDILEKGL-INNENIPNLVGTLT- 1015
Qy 483 TFLTPINGF--GLVVDENSRLVLTCKSYLRETLATDLSNKETKLIYPNGFISNIVEN 540
Db 1016 TNLIVKNPFVYKELTVDOKOKI-----NNFTNIIPT 1046
Qy 541 GNLEGENLEPMKANNAVYDHTGNGTV-----LYVHEDGRFSQFIGDKL-KLTKY 594
Db 1047 ----TPNLTLYKEIRKQAFEFLLNNINKILVDPKNTLLILNDG-INKLISNILEPOLST-- 1099
Qy 595 VIOYIVGKAALYLKDEKNGDYIEETNNELEDFQAVTKRFTIGTSSRVHLIFTSONGE 654
Db 1100 LIEILDNDK---IKD-----QDFIDVIKIFIDNLDPNKLFVNIKSNNO 1140
Qy 655 -----EAFGNGFTISEIRPSEBELSPELIKSDAWGSGGTWISGNSLAINSVNGTFR 707
Db 1141 TTDSTTLNQFYFKFKLN-LEPKLIF--DLIKN-----LINSPIKLVNDKKNKIK 1188
Qy 708 ---QNTLSGSYSTYS-----MNP-----NNGPGKVTIRNSREAVFERSY 744
Db 1189 IESNKAKIKSILITTSVINIPENSMLMNFENNQLSQLFSSIDLFPNINLNSQORLNFPAKAI 1248
Qy 745 LQPSKXYISEKFTTTNN 762
Db 1249 VELNK---EKLSNLIN 1263

Search completed: May 15, 2006, 20:44:04
Job time : 49 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 15, 2006, 20:36:11 ; Search time 234 Seconds
(without alignments)
2369.851 Million cell updates/sec

Title: US-10-698-096-17
Perfect score: 3995
Sequence: 1 MOKNNKLSVKALPSFIDYFN.....VELSPASSRGVINFDPFSIK 786

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3527	88.3	787	Q5JZY8_BACTU	Q5JZY8_Bacillus th
2	3243.5	81.2	788	Q5JYZ0_BACTU	Q5JYZ0_Bacillus th
3	3176.5	79.5	789	Q5B133_BACTU	Q5B133_Bacillus th
4	3175.5	79.5	789	Q5XPO5_BACTU	Q5XPO5_Bacillus th
5	3175.5	79.5	789	Q788G2_BACTU	Q788G2_Bacillus th
6	3175.5	79.5	789	Q788G2_BACTU	Q788G2_Bacillus th
7	3175.5	79.5	789	Q788G2_BACTU	Q788G2_Bacillus th
8	3171.5	79.4	789	Q58X12_BACTU	Q58X12_Bacillus th
9	3171.5	79.4	789	Q58X12_BACTU	Q58X12_Bacillus th
10	3168.5	79.3	789	Q45792_BACTU	Q45792_Bacillus th
11	3168.5	79.3	789	Q45792_BACTU	Q45792_Bacillus th
12	3163.5	79.2	789	Q4VY70_BACTU	Q4VY70_Bacillus th
13	3160	79.1	786	Q4U3F5_BACTU	Q4U3F5_Bacillus th
14	3159.5	79.1	789	Q5JZY9_BACTU	Q5JZY9_Bacillus th
15	3156.5	79.0	789	Q4U3F4_BACTU	Q4U3F4_Bacillus th
16	3113.5	77.9	789	Q45793_BACTU	Q45793_Bacillus th
17	2879.5	72.1	657	Q75152_BACTO	Q75152_Bacillus th
18	2419	60.6	803	Q93D79_BACTU	Q93D79_Bacillus th
19	840	21.0	190	Q5PXG4_BACTU	Q5PXG4_Bacillus th
20	807.5	20.2	183	Q93D74_BACTU	Q93D74_Bacillus th
21	783	19.6	175	Q93D77_BACTU	Q93D77_Bacillus th
22	770	19.3	166	Q93D75_BACTU	Q93D75_Bacillus th
23	662	16.6	147	Q6S551_BACTU	Q6S551_Bacillus th
24	609	15.2	140	Q6S550_BACTU	Q6S550_Bacillus th
25	604	15.1	136	Q6S547_BACTU	Q6S547_Bacillus th
26	535	13.4	121	Q6S549_BACTU	Q6S549_Bacillus th
27	313	7.8	80	Q6S548_BACTU	Q6S548_Bacillus th
28	247.5	6.2	1705	Q78BA8_PLAYO	Q78BA8_plasmodium
29	245	6.1	2965	Q26216_9APIC	Q26216_plasmodium
30	245	6.1	2965	Q8WRS5_PLAFA	Q8WRS5_plasmodium
31	242.5	6.1	5767	Q81525_PLAFA	Q81525_plasmodium

32	235	5.9	2868	2	Q5DSD9_PLAVI	Q5DSD9_plasmodium
33	233	5.8	1081	2	Q7RF07_PLAYO	Q7RF07_plasmodium
34	233	5.8	2869	2	Q7KE73_PLAFA	Q7KE73_plasmodium
35	231.5	5.8	2649	2	Q7BAS7_PLAYO	Q7BAS7_plasmodium
36	231	5.8	2770	2	Q7YUE9_PLAFA	Q7YUE9_plasmodium
37	231	5.8	2957	2	Q8WRS6_PLAFA	Q8WRS6_plasmodium
38	229.5	5.7	2867	1	RBP2_PLAVB	Q00799_plasmodium
39	229.5	5.7	2881	2	Q6YA78_PLARB	Q6YA78_plasmodium
40	229	5.7	880	2	Q5HVS9_CAMUR	Q5HVS9_campylobact
41	227	5.7	2297	2	Q8WP99_PLAFA	Q8WP99_plasmodium
42	226	5.7	1958	2	Q4YBL9_PLAFA	Q4YBL9_plasmodium
43	226	5.7	2110	2	Q54BP1_DICTDI	Q54BP1_dicystostei
44	225.5	5.6	2785	2	Q4PZ10_9APIC	Q4PZ10_plasmodium
45	224.5	5.6	1665	2	Q6YA77_PLARB	Q6YA77_plasmodium

ALIGNMENTS

RESULT 1	ID	Q5JZY8_BACTU	PRELIMINARY;	PRT;	787 AA.
AC	Q5JZY8;	Q5JZY8_BACTU			
DT	10-MAY-2005	(TREMBLrel. 30, Created)			
DT	10-MAY-2005	(TREMBLrel. 30, Last sequence update)			
DT	10-MAY-2005	(TREMBLrel. 30, Last annotation update)			
DE	Ispc protein.				
OS	Bacillus thuringiensis.				
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;				
OX	Bacillus cereus group.				
RN	NCBI_TaxID=1428;				
RP	[1]				
RA	NUCLEOTIDE SEQUENCE.				
RT	van Rie J., Arnaut G., Boers A., Damme N.;				
RT	"Genes encoding insecticidal secreted proteins from Bacillus thuringiensis."				
RL	Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AJ872072; CA14327.1; -; Genomic DNA.				
DR	GO; GO:0016798; P:hydrolyase activity; acting on glycosyl bonds; IEA.				
DR	GO; GO:0016491; F:oxidoreductase activity; IEA.				
DR	GO; GO:0005975; P:carbohydrate metabolism; IEA.				
DR	InterPro; IPR003305; CBM_CenC.				
DR	Pfam; PF02018; CBM_4_9; I.				
KW	Oxidoreductase.				
SQ	SEQUENCE 787 AA; 88359 MW; 0B1AF7876F3D62 CRC64;				
Query Match	88.3%; Score 3527; DB 2; length 787;				
Best local similarity	87.5%; Pred. No. 6.5e-157;				
Matches	685; Conservative 43; Mismatches 55; Indels 0; Gaps 0;				
QY	4	NNKLSVRLPSPFIYFNGIYGFATGIDIMMIRKNTGDLTDEIKNOQLNEISGK	63		
DB	5	NTKLNARLPSPFIYFNGIYGFATGIDIMMIRKNTGDLTDEIKNOQLNEISGK	64		
QY	64	LDGVNGSLNDLAQGNIDTELSEKILKIANQNVNLDVNTKRLAINMLMTYLPKITSM	123		
DB	65	LDGVNGSLNDLAQGNIDTELSEKILKIANQNVNLDVNTKRLAINMLMTYLPKITSM	124		
QY	124	LSDVKNQYALGLQIEYLSKQKEISDKLDVINNVNLINSTLTETPAYORIKTYVNEKE	183		
DB	125	LSDVKNQYALGLQIEYLSKQKEISDKLDVINNVNLINSTLTETPAYORIKTYVNEKE	184		
QY	184	ALTEATETNLTQKDDSHDTDLDELTLTELAKSVTKQVDGFEFFYNTFHDVMIQNNLF	243		
DB	185	ELTFATETTLTKVKKDGPADILDELTLTELAKSVTKQVDGFEFFYNTFHDVMIQNNLF	244		
QY	244	GRSLAKTASSELIAKENKTSGSEGVNYPFLIVTALQAKAPLTLTCKRLGLADIDYT	303		
DB	245	GRSLAKTASSELIAKENKTSGSEGVNYPFLIVTALQAKAPLTLTCKRLGLADIDYT	304		
QY	304	PIMNEHLNKEKEFRVNIPLTLSTFSPNPNYERKAGSDKAKIMEAKPGYALVGFEISK	363		
DB	305	SIMNEHLNKEKEFRVNIPLTLSTFSPNPNYERKAGSDKAKIMEAKPGYALVGFEISM	364		

```
QY 364 DSIATLVKVOAKLKHNYQIDDKDLSSEIVYGDIDKLCPPDSEOMYTNKIAFENEYITK 423
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 365 DSNMIVLAKYQAKLKQDQVQDKDLSSEIVYGDIMKLCPPDSEQIYTNMIAFENEYITK 424
QY 424 IAFKKLNSLRVEVTANFYDSSTGDIIDLNKKKIBSSBAEFSMLNANDGVYMPIGTISET 483
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 425 LTFKKKNSLRVEVTANFYDSSTGDMIDNKKKIBSSBAEFSMLNANDGVYMPIGTISET 484
QY 484 FLTPINGFGLVVDNSRLVLTCKSYLRRETLATDLSNKKTKLIVPENGFSINIVENGNL 544
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 485 FLTPINGFGLVVDNSRLVLTCKSYLRRETLATDLSNKKTKLIVPENGFSINIVENGNL 544
QY 544 EGENLEPMKANNKAAVYDHFGVNGTKVLYVHEDGESQFIDGKLKATEYVIOYIYKKG 603
Db 545 EGENLEPMKANNKAAVYDHFGVNGTKVLYVHEDGESQFIDGKLKATEYVIOYIYKKG 604
QY 604 AAIYLDKDKNGDYIYEETNNLEDFQAVTKRFTIGTDSRVHLIFTSQNGEBAFGNFI 663
Db 605 AAIYLDKDKNGDYIYEETNNLEDFQAVTKRFTIGTDSRVHLIFTSQNGEBAFGNFI 664
QY 664 SEIRPSEELSPELIKSDAWGSGTWISGNSLINSNVNGTFRQNLSESYSTYSNMFN 723
Db 665 SEIRPSEELSPELIKSDAWGSGTWISGNSLINSNVNGTFRQNLSESYSTYSNMFN 724
QY 724 VNGFGKTYINSREVFERSYLOFSSKYISEKFTTTNTNGLVYELSRASRGVINFQDF 783
Db 725 ITGFGKTYINSREVLFEKNSQSLEKFTTTAANTGFIYELSRGOGGNTTRDF 784
QY 784 SIK 786
    |||
Db 785 SIK 787
```

RESULT 2

```
Q5JZ20_BACTU PRELIMINARY; PRT; 788 AA.
ID Q5JZ20_BACTU PRELIMINARY; PRT; 788 AA.
AC Q5JZ20;
DT 10-MAY-2005 (Tremblrel. 30, Created)
DT 10-MAY-2005 (Tremblrel. 30, Last sequence update)
DT 10-MAY-2005 (Tremblrel. 30, Last annotation update)
DE 18p3a protein.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1428;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Van Rie J., Arnaut G., Boets A., Damme N.;
RT "Gene encoding insecticidal secreted proteins from Bacillus thuringiensis.";
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
RL EMBL: AJ812070; CAI43275.1; -; Genomic_DNA.
DR GO: GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO: GO:0016491; F:oxidoreductase activity; IEA.
DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro: IPR003305; CBM Cenc.
DR Pfam: PF02018; CBM_4_9; I.
KW Oxidoreductase.
SQ SEQUENCE 788 AA; 88037 MW; 5A7314AA1D4A60B8 CRC64;
```

```
Query Match 81.2%; Score 3243.5; DB 2; Length 788;
Best Local Similarity 80.9%; Pred. No. 1.2e-143;
Matches 634; Conservative 65; Mismatches 84; Indels 1; Gaps 1;
```

QY 4 NNTKLSVATLPSFIDYENGIGFATGIDIMNMIFKNTGTGDLTLDLTKKQQLINISGK 63
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 5 NTKLNAALPSFIDYENGIGFATGIDIMNMIFKNTGTGDLTLDLTKKQQLINISGK 64
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 64 LDGVNGSLNDLTAQGNIDTELSEKILKIANEONVLDVNTKLDALINMLNTYVPIKITSM 123
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 65 LDGVNGSLNDLTAQGNIDTELSEKILKIANEONVLDVNTKLDALINMLNTYVPIKITSM 124

```
QY 124 LSDVMKQNYALGLQIEYLSKOLKEISDKLDVINNVNLINSTEITPAVORIKYVNEKFE 183
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 125 LSDVMKQNYALSLQIEYLSKQLQEIISDKLDVINNVNLINSTEITPAVORIKYVNEKFE 184
QY 184 ALTSATETNLKTYQDSSHDIDELTELTLASVTKNDYDGEFYANTFHDVIGNLF 243
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 185 ELTFATETTLKVKQDSSPADIDELTELTLAKSVTKNDVDGEPFYANTFHDVIGNLF 244
QY 244 GRSALKTASELIKENIKTSGSEGVNPNLYLVTLLQAQAFLLTTCRLLGLADIY 303
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 245 GRSALKTASELIKENIKTSGSEGVNPNLYLVTLLQAQAFLLTTCRLLGLADIY 304
QY 304 PINNEHLNKEKEFRVNIIPLTLSNTPNPNYERKAGSGDXAKIMEAKPGYALVGEPIK 363
Db 305 SINNEHLNKEKEFRVNIIPLTLSNTPNPNYERKAGSGDXAKIMEAKPGYALVGEPIK 364
QY 364 DSIATLVKVOAKLKHNYQIDDKDLSSEIVYGDIDKLCPPDSEOMYTNKIAFENEYITK 423
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 365 DSIATLVKVOAKLKHNYQIDDKDLSSEIVYGDIDKLCPPDSEOMYTNKIAFENEYITK 424
QY 424 IAFKKLNSLRVEVTANFYDSSTGDIIDLNKKKIBSSBAEFSMLNANDGVYMPIGTISET 483
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 425 IAFKKLNSLRVEVTANFYDSSTGDIIDLNKKKIBSSBAEFSMLNANDGVYMPIGTISET 484
QY 484 FLTPINGFGLVVDNSRLVLTCKSYLRRETLATDLSNKKTKLIVPENGFSINIVENGNL 543
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 485 FLTPINGFGLVVDNSRLVLTCKSYLRRETLATDLSNKKTKLIVPENGFSINIVENGNL 544
QY 544 EGENLEPMKANNKAAVYDHFGVNGTKVLYVHEDGESQFIDGKLKATEYVIOYIYKKG 603
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 545 EGENLEPMKANNKAAVYDHFGVNGTKVLYVHEDGESQFIDGKLKATEYVIOYIYKKG 604
QY 604 AAIYLDKDKNGDYIYEETNNLEDFQAVTKRFTIGTDSRVHLIFTSQNGEBAFGNFI 663
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 605 PSIHLDKENTGYIHEEDTNANLKOYQITRFTTGTDDAKVYIILKSQNGDEAMGDKFTI 664
QY 664 SEIRPSEELSPELIKSDAWGSGTWISGNSLINSNVNGTFRQNLSESYSTYSNMFN 723
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 665 LEIKPADLSPELINPNNSWITTPGASISGNKLFILGTGTGRQSLNSYSTYSISFT 724
QY 724 VNGFGKTYINSREVFERSYLOFSSKYISEKFTTTNTNGLVYELSRASRGVINFQDF 782
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 725 ASGPFNVTYNSREVLFEKNSQSLEKFTTTAANTGFIYELSRGOGGNTTRDF 784
QY 783 SIK 786
    |||
Db 785 VSIX 788
```

RESULT 3

```
Q58I33_BACTU PRELIMINARY; PRT; 789 AA.
ID Q58I33_BACTU PRELIMINARY; PRT; 789 AA.
AC Q58I33;
DT 10-MAY-2005 (Tremblrel. 30, Created)
DT 10-MAY-2005 (Tremblrel. 30, Last sequence update)
DT 10-MAY-2005 (Tremblrel. 30, Last annotation update)
DE Vegetative insecticidal protein.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1428;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Cai J., Xiao L.;
RT "Bacillus thuringiensis strain 9816C vegetative insecticidal protein gene.";
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY945939; AAY49395.1; -; Genomic_DNA.
KW Oxidoreductase.
SQ SEQUENCE 789 AA; 88675 MW; 9F13448BA7C7AA CRC64;
```

Query Match 79.5%; Score 3176.5; DB 2; Length 789;

Best Local Similarity 78.6%; Pred. No. 1.7e-140;
Matches 621; Conservative 70; Mismatches 94; Indels 5; Gaps 3;

```

QY 1 MOKNN-KLSVKALPSFIDYFNGIYGATGICDIDMMNIFKTMNGDITLDEILKNOOLNE 59
DB 1 MOKNNKTLSTRALPSFIDYFNGIYGATGICDIDMMNIFKTMNGDITLDEILKNOOLNE 60
QY 60 ISGKLDGVNGSLNDLIAQGNLDTLSKEILKIANEQNKVLDVNTKLDAINMLMTYLPK 119
DB 61 ISGKLDGVNGSLNDLIAQGNLDTLSKEILKIANEQNKVLDVNTKLDAINMLMTYLPK 120
QY 120 ITSMUSDVWKONYALGLQIEYLSKQKKEISDKLDVINNVNLINSTLITTPAYQRIKYVN 179
DB 121 ITSMUSDVWKONYALSLQIEYLSKQKKEISDKLDVINNVNLINSTLITTPAYQRIKYVN 180
QY 180 EKFEALTSATETNLTCKDSSHTDILDELTELTELAKSVTKNDVGFEEYNTFHDVWG 239
DB 181 EKFEELTRATETTSKVKDGSPPADILDELTELTELAKSVTKNDVGFEEYNTFHDVWG 240
QY 240 NNLFGRSALKTASSELIAKENLKTSGSEVGNVNFILVLTALQAKAFLLTTCRKLGLAD 299
DB 241 NNLFGRSALKTASSELITKENVKTSGSEVGNVNFILVLTALQAKAFLLTTCRKLGLAD 300
QY 300 IDYTPINMEHLNKEKEEPRVNIPLTSLNTPSNPTEKARGSDKAKIIMEARPYALVGF 359
DB 301 IDYTSINMEHLNKEKEEPRVNIPLTSLNTPSNPNTAKVGSDEDAKMIVEAKPGHALIGF 360
QY 360 EISKOSIAYLVKYOAKLKHNYOIKDLSSEIYVGDIDKLCPDQSEOMYTNKIAFPNEY 419
DB 361 EISNDSTIVLVKYTEAKLKHNYOIKDLSSEIYVGDIDKLCPDQSEOMYTNKIAFPNEY 420
QY 420 VITKIDFTKKNKTLAREYVLANFYDSGTGIDILANKKIESSSEAFSEMLNANDGVYMPIGT 479
DB 421 VITKIDFTKKNKTLAREYVLANFYDSGTGIDILANKKIESSSEAFSEMLNANDGVYMPIGT 480
QY 480 ISEFTLPINGFGLVVDENSRILVLTCKSYLRETLTADLSNKEKTLIVPPNGFISNIVE 539
DB 481 ISEFTLPINGFGLVVDENSRILVLTCKSYLRETLTADLSNKEKTLIVPPNGFISNIVE 540
QY 540 NGNLEGENLEBPKANNKNAAYDHTGCVNGTKVLYVHDEGSPQIFGDKLAKTEVVIQYI 599
DB 541 NGNLEGENLEBPKANNKNAAYDHTGCVNGTKVLYVHDEGSPQIFGDKLAKTEVVIQYI 600
QY 600 VKGKAAYLVKDEKNDGYIYEETNNLEDPQAVTKAFITGDSRVHLIFTSONGEBAFGG 659
DB 601 VKGKSIHLKDEKNDGYIYEETNNLEDPQAVTKAFITGDSRVHLIFTSONGEBAFGG 660
QY 660 NFIISEIRPSEBELSPELIKSDAVVSGQTVISGNSLNINSNVNGTFRQNTSLSESYTYS 719
DB 661 NFIISEIRPSEBELSPELIKSDAVVSGQTVISGNSLNINSNVNGTFRQNTSLSESYTYS 720
QY 720 MNFVNGGKVTIINSREVPERSEYLOFSSKYSISEKFTTTNNNGLVYELSRASS--RG 776
DB 721 VYFVSQDANVRINSREVLEPKRYMS-GADVSEMFTTKEKONFYIELSQGNMLYGGP 779
QY 777 VINFGDFSIK 786
DB 780 IVHFYDVSIK 789

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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=wy-197;
RA Li J., Yan J., Yuan Z.,
RT "Cloning and expression of vip3a gene from *Bacillus thuringiensis*
RT strain wy-197."
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY743436; AAU89707.1; -; Genomic DNA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR003305; CEM_CenC.
DR Pfam; PF02018; CEM_4_9; 1.
KW Oxidoreductase.
SQ SEQUENCE 789 AA; 88642 MW; 6322FD4A4EBCT0D4 CRC64;

Query Match 79.5%; Score 3175.5; DB 2; Length 789;
Best Local Similarity 78.6%; Pred. No. 1.8e-140;
Matches 621; Conservative 70; Mismatches 94; Indels 5; Gaps 3;

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QY 1 MOKNN-KLSVKALPSFIDYFNGIYGATGICDIDMMNIFKTMNGDITLDEILKNOOLNE 59
DB 1 MOKNNKTLSTRALPSFIDYFNGIYGATGICDIDMMNIFKTMNGDITLDEILKNOOLNE 60
QY 60 ISGKLDGVNGSLNDLIAQGNLDTLSKEILKIANEQNKVLDVNTKLDAINMLMTYLPK 119
DB 61 ISGKLDGVNGSLNDLIAQGNLDTLSKEILKIANEQNKVLDVNTKLDAINMLMTYLPK 120
QY 120 ITSMUSDVWKONYALGLQIEYLSKQKKEISDKLDVINNVNLINSTLITTPAYQRIKYVN 179
DB 121 ITSMUSDVWKONYALSLQIEYLSKQKKEISDKLDVINNVNLINSTLITTPAYQRIKYVN 180
QY 180 EKFEALTSATETNLTCKDSSHTDILDELTELTELAKSVTKNDVGFEEYNTFHDVWG 239
DB 181 EKFEELTRATETTSKVKDGSPPADILDELTELTELAKSVTKNDVGFEEYNTFHDVWG 240
QY 240 NNLFGRSALKTASSELIAKENLKTSGSEVGNVNFILVLTALQAKAFLLTTCRKLGLAD 299
DB 241 NNLFGRSALKTASSELITKENVKTSGSEVGNVNFILVLTALQAKAFLLTTCRKLGLAD 300
QY 300 IDYTPINMEHLNKEKEEPRVNIPLTSLNTPSNPTEKARGSDKAKIIMEARPYALVGF 359
DB 301 IDYTSINMEHLNKEKEEPRVNIPLTSLNTPSNPNTAKVGSDEDAKMIVEAKPGHALIGF 360
QY 360 EISKOSIAYLVKYOAKLKHNYOIKDLSSEIYVGDIDKLCPDQSEOMYTNKIAFPNEY 419
DB 361 EISNDSTIVLVKYTEAKLKHNYOIKDLSSEIYVGDIDKLCPDQSEOMYTNKIAFPNEY 420
QY 420 VITKIDFTKKNKTLAREYVLANFYDSGTGIDILANKKIESSSEAFSEMLNANDGVYMPIGT 479
DB 421 VITKIDFTKKNKTLAREYVLANFYDSGTGIDILANKKIESSSEAFSEMLNANDGVYMPIGT 480
QY 480 ISEFTLPINGFGLVVDENSRILVLTCKSYLRETLTADLSNKEKTLIVPPNGFISNIVE 539
DB 481 ISEFTLPINGFGLVVDENSRILVLTCKSYLRETLTADLSNKEKTLIVPPNGFISNIVE 540
QY 540 NGNLEGENLEBPKANNKNAAYDHTGCVNGTKVLYVHDEGSPQIFGDKLAKTEVVIQYI 599
DB 541 NGNLEGENLEBPKANNKNAAYDHTGCVNGTKVLYVHDEGSPQIFGDKLAKTEVVIQYI 600
QY 600 VKGKAAYLVKDEKNDGYIYEETNNLEDPQAVTKAFITGDSRVHLIFTSONGEBAFGG 659
DB 601 VKGKSIHLKDEKNDGYIYEETNNLEDPQAVTKAFITGDSRVHLIFTSONGEBAFGG 660
QY 660 NFIISEIRPSEBELSPELIKSDAVVSGQTVISGNSLNINSNVNGTFRQNTSLSESYTYS 719
DB 661 NFIISEIRPSEBELSPELIKSDAVVSGQTVISGNSLNINSNVNGTFRQNTSLSESYTYS 720
QY 720 MNFVNGGKVTIINSREVPERSEYLOFSSKYSISEKFTTTNNNGLVYELSRASS--RG 776
DB 721 VYFVSQDANVRINSREVLEPKRYMS-GADVSEMFTTKEKONFYIELSQGNMLYGGP 779
QY 777 VINFGDFSIK 786
DB 780 IVHFYDVSIK 789

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Db 780 IVAHYDVSIR 789

RESULT 5

O938G2_BACTU PRELIMINARY; PRT; 789 AA.

AC Q79SG2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Vegetative insecticidal protein.
GN Name=vip3;
OS *Bacillus thuringiensis serovar lewisii*.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC *Bacillus cereus* group.
OX NCBI_TaxID=169759;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=YBT-833;
RA Cai Q., Liu Z., Sun M., Yu Z.;
RT "Vegetative insecticidal protein gene vip3 from *Bacillus thuringiensis serovar lewisii* strain YBT-833."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY044227; MAK95326.1; -; Genomic DNA.
DR GO: GO:0016491; F:oxidoreductase activity; IEA.
DR InterPro: IPR003305; CBM_Cenc.
DR Pfam: PF02018; CBM_4_9; I.
KM Oxidoreductase.
SQ SEQUENCE 789 AA; 88671 MM; 9DD746486823C7AE CRC64;

Query Match 79.5%; Score 3175.5; DB 2; Length 789;
Best Local Similarity 78.6%; Pred. No. 1.8e-140;
Matches 621; Conservative 70; Mismatches 94; Indels 5; Gaps 3;

QY 1 MOKNN-ELSYKALPSFIDYNGYGFATGKIDIMNMFKMTGSDLLDELTKNQOLNE 59
DB 1 MNKNNTSTRALPSFIDYNGYGFATGKIDIMNMFKMTGSDLLDELTKNQOLNE 60
QY 60 ISGKLDGVNSLNDLLAQNLDELTELSEIKIANEQNKVINDVTKLDAINLMNTYLPK 119
DB 61 ISGKLDGVNSLNDLLAQNLDELTELSEIKIANEQNKVINDVTKLDAINLMNTYLPK 120
QY 120 ITSMLSVVKONTALGQIETLSKQKEISDKLDVINNVNLINSTLETPAYORIKYVN 179
DB 121 ITSMLSVVKONTALGQIETLSKQKEISDKLDVINNVNLINSTLETPAYORIKYVN 180
QY 180 EKPEALTSATETNLTQKQSSHTDIDELTELTELASVKNDVGEFEYLNTHFDWMIG 239
DB 181 EKPEALTSATETNLTQKQSSHTDIDELTELTELASVKNDVGEFEYLNTHFDWMIG 240
QY 240 NNLFGSALXTASBELAKENLKTSGSEVGVNVPFLVLTALQAKAPLTLTTCRKLGLAD 239
DB 241 NNLFGSALXTASBELAKENLKTSGSEVGVNVPFLVLTALQAKAPLTLTTCRKLGLAD 300
QY 300 IDYTPINNEHLNKEKEFRVNIPTLSNTSPNPEYAKSGSDKDAKIMEAKGVALVGF 359
DB 301 IDYTPINNEHLNKEKEFRVNIPTLSNTSPNPEYAKSGSDKDAKIMEAKGVALVGF 360
QY 360 EISKDSIAVLKVVYQAKLKHNYQIDKDSLRIYVGDIDKLCPPDSEOMYTNKAPAPNEY 419
DB 361 EISKDSIAVLKVVYQAKLKHNYQIDKDSLRIYVGDIDKLCPPDSEOMYTNKAPAPNEY 420
QY 420 VITKIAFTKLNLSRYEVNTANFYDSTGDIIDLNKKKLESSEAEFSMANNNDGVMPIGT 479
DB 421 VITKIDTTPKMKTLRYEVNTANFYDSTGDIIDLNKKKLESSEAEFSMANNNDGVMPIGT 480
QY 480 ISETFLTPINGFGLVVDENSLVTLTKCKSYKRETLATDLSNKETKLIIPNGEISNIVE 539
DB 481 ISETFLTPINGFGLVVDENSLVTLTKCKSYKRETLATDLSNKETKLIIPNGEISNIVE 540
QY 540 NGNLEGENLEPMWANNKQAVVDHTGVNGTKLVYHEDGEFSOPIGKCLKKTEYVQYI 599
DB 541 NGNLEGENLEPMWANNKQAVVDHTGVNGTKLVYHEDGEFSOPIGKCLKKTEYVQYI 600

QY 600 VKGKAAILKDEKNGDIYEETNNLEDFQAVTKRFTGTDSRVHLIFTSQNGEAFGC 659
DB 601 VKGKPSHLKDEKNGDIYHEDTNNLEDFQAVTKRFTGTGTDLKGVHLILKSQNGDEAMGD 660
QY 660 NFIISIRPSEELLSPELIKSDAMVGSQGTWISGNSLNTSVNNGTFRRONLSBSYSTYS 719
DB 661 NFIILSIRPSEELLSPELIKSDAMVGSQGTWISGNSLNTSVNNGTFRRONLSBSYSTYS 720
QY 720 MNFNNGVFGKVTLRNSREVVEERSYLOFSKYSSEKFTTTNTTGLVYELSRASS--RG 776
DB 721 VYFVSQDANVRIRNSREVVEERSYLOFSKYSSEKFTTTNTTGLVYELSRASS--RG 779
QY 777 VINFGDPSIK 786
DB 780 IVAHYDVSIR 789

RESULT 6

O938Z1_BACTU PRELIMINARY; PRT; 789 AA.

AC O938Z1; O8L2N0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Vegetative insecticidal protein Vip3A (Vegetative insecticidal protein Vip3V).
GN Name=vip3A; Synonyms=vip3A-WB5, vip3V;
OS *Bacillus thuringiensis*.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC *Bacillus cereus* group.
OX NCBI_TaxID=1428;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=8101, and 611;
RA Chen J., Yu J., Pang Y., Tang L.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Wu Y., Guan X.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=WB 50;
RA PubMed=15604775; DOI=10.1023/B:BILE.0000045645.45536.3f;
RX Wu Z.L., Guo W.Y., Qiu J.Z., Huang T.P., Li X.B., Guan X.;
RT "Cloning and localization of vip3A gene of *Bacillus thuringiensis*.";
RL Biotechnol. Lett. 26:1425-1428(2004).
RN [4]

NUCLEOTIDE SEQUENCE.

RP MEDLINE=2244722; PubMed=12356474; DOI=10.1016/S1046-5928(02)00515-6;
RA Does V.A., Anup Kumar K., Jayakumar R., Sekar V.;
RT "Cloning and expression of the vegetative insecticidal protein (vip3v) gene of *Bacillus thuringiensis* in *Escherichia coli*.";
RL Protein Expr. Purif. 26:82-88(2002).
RN [5]

NUCLEOTIDE SEQUENCE.

RC STRAIN=C9;
RA Liu R., Song F., Zhang J.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY074707; AAL69543.1; -; Genomic DNA.
DR EMBL: AF500478; AAM22456.2; -; Genomic DNA.
DR EMBL: AF295778; AAP51131.1; -; Genomic DNA.
DR EMBL: AF373030; AAN60738.1; -; Genomic DNA.
DR EMBL: AY489126; AAR36859.1; -; Genomic DNA.
DR EMBL: AY074708; AAL69544.1; -; Genomic DNA.
DR GO: GO:0016491; F:oxidoreductase activity; IEA.
DR InterPro: IPR003305; Cenc carb_bd.
DR Pfam: PF02018; CBM_4_9; I.
KM Oxidoreductase.
SQ SEQUENCE 789 AA; 88672 MM; 9DD746486823C7AE CRC64;

Query Match 79.5%; Score 3175.5; DB 2; Length 789;

Best Local Similarity 78.6%; Pred. No. 1.8e-140;
Matches 621; Conservative 70; Mismatches 94; Indels 5; Gaps 3;

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QY 1 MOKN-KLSVKALPSFIDYFNGIYGFATGKIDIMNIPFTNGGDLTDEILKNOQLNE 59
DB 1 MKNKNTKSTRALPSFIDYFNGIYGFATGKIDIMNIPFTNGGDLTDEILKNOQLNE 60
QY 60 ISGKLDGVNGSLNDLLAOGNLDTELSKEILKIANEQNVLDVNTKLDANIMLANTYLPK 119
DB 61 ISGKLDGVNGSLNDLLAOGNLDTELSKEILKIANEQNVLDVNTKLDANIMLANTYLPK 120
QY 120 ITSMUSDVWKONVYALGLQIEYLSKQLEISDKLDVINNVNLINSTLTETTPAYQRIKYVN 179
DB 121 ITSMUSDVWKONVYALGLQIEYLSKQLEISDKLDVINNVNLINSTLTETTPAYQRIKYVN 180
QY 180 EKFEALTSAETNLTCKODSSHDTLDDELTELTELAKSVTKNDVDGFEFYLTFFHDVWG 239
DB 181 EKFEALTSAETNLTCKODSSHDTLDDELTELTELAKSVTKNDVDGFEFYLTFFHDVWG 240
QY 240 NNLFGRSALKTASBLIAKENLKTSGSEVGAVNFFLVTALQAKAFLLTTCKRLGLAD 299
DB 241 NNLFGRSALKTASBLIAKENLKTSGSEVGAVNFFLVTALQAKAFLLTTCKRLGLAD 300
QY 300 IYTPIMNEHLNKEKEEFPNVNLLPTLSNTPSNPNYKARAGSDKAKIIMEAKPGYALVGF 359
DB 301 IYTPIMNEHLNKEKEEFPNVNLLPTLSNTPSNPNYKARAGSDKAKIIMEAKPGYALVGF 360
QY 360 EISKOSIAYLKYYOAKLKHNOQIDKOSISEIYVGIDILCLPDQSEQMYTNTKIAFPNEY 419
DB 361 EISKOSIAYLKYYOAKLKHNOQIDKOSISEIYVGIDILCLPDQSEQMYTNTKIAFPNEY 420
QY 420 VITKIAFTKQNSLREYVLANFYDSSTGDIIDLNKKKIESSEABFSMLNANDGVYMPIGT 479
DB 421 VITKIDFTKQKMTLREYVLANFYDSSTGDIIDLNKKKIESSEABFSMLNANDGVYMPIGT 480
QY 480 ISETFLTPINGGLVVDENSRLLVTLTCKSYLRETLATDLSNKETKLIIPPNGFISNIYE 539
DB 481 ISETFLTPINGGLVVDENSRLLVTLTCKSYLRETLATDLSNKETKLIIPPNGFISNIYE 540
QY 540 NGNLEGENLEFPWKANNKAYVDHTGVNGTGYLVYHEDGEPGQFIDKAKLKTREYVIOYT 599
DB 541 NGNLEGENLEFPWKANNKAYVDHTGVNGTGYLVYHEDGEPGQFIDKAKLKTREYVIOYT 600
QY 600 VKGKAALYLDKDEKNDYIYEETNNLEDFQAVTKKPFITGTSSRYHLIFTSONGEBAFG 659
DB 601 VKGKSIHLKDEKNTGYIHYEDTNNLEDFQAVTKKPFITGTDLKGYVLLKSGQGBEAMGD 660
QY 660 NFIISEIRPSEELSPBLIKSDAWGSGQTIWISGNSLINSVNGTFRONTLSLESYSTYS 719
DB 661 NFIISEIRPSEELSPBLIKSDAWGSGQTIWISGNSLINSVNGTFRONTLSLESYSTYS 720
QY 720 MNFVNGFGKTYTINSREVFERSYLOPSSKYISEKFTTTNTNGLYELSPASS--RG 776
DB 721 VYFVSVDANVIRINSREVLFEKRYMS-GAKDVSEMFYTKPEKONFYIELSGNNLYGCP 779
QY 777 VINFGDPSIK 786
DB 780 IVHFYDVSIK 789

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RESULT 7
058x12_BACTU PRELIMINARY; PRT: 789 AA.
AC 058x12-
DT 10-MAY-2005 (TREMBLrel. 30, Created)
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
DE Vegetative insecticidal protein.
GN Name=vi3JB;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
NCBI_TaxID=1428;

RN [1]
RA NUCLEOTIDE SEQUENCE.
RP Abdelkefi Mestarti L., Tounsi S., Jaoua S.;
RT "Characterization of a novel vip3-type gene from Bacillus
RT thuringiensis and evidence of its presence on a large plasmid.";
RL FEMS Microbiol. Lett. 244:353-358 (2005).
DR EMBL; AY39665; AA65132.1; -; Genomic_DNA.
KW Oxidoreductase.
SQ SEQUENCE 789 AA; 88671 MW; EC5355939F676CA CRC64;

Query Match 79.4%; Score 3173.5; DB 2; Length 789;
Best Local Similarity 78.5%; Pred. No. 2.3e-140;
Matches 620; Conservative 71; Mismatches 94; Indels 5; Gaps 3;

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QY 1 MOKN-KLSVKALPSFIDYFNGIYGFATGKIDIMNIPFTNGGDLTDEILKNOQLNE 59
DB 1 MKNKNTKSTRALPSFIDYFNGIYGFATGKIDIMNIPFTNGGDLTDEILKNOQLNE 60
QY 60 ISGKLDGVNGSLNDLLAOGNLDTELSKEILKIANEQNVLDVNTKLDANIMLANTYLPK 119
DB 61 ISGKLDGVNGSLNDLLAOGNLDTELSKEILKIANEQNVLDVNTKLDANIMLANTYLPK 120
QY 120 ITSMUSDVWKONVYALGLQIEYLSKQLEISDKLDVINNVNLINSTLTETTPAYQRIKYVN 179
DB 121 ITSMUSDVWKONVYALGLQIEYLSKQLEISDKLDVINNVNLINSTLTETTPAYQRIKYVN 180
QY 180 EKFEALTSAETNLTCKODSSHDTLDDELTELTELAKSVTKNDVDGFEFYLTFFHDVWG 239
DB 181 EKFEALTSAETNLTCKODSSHDTLDDELTELTELAKSVTKNDVDGFEFYLTFFHDVWG 240
QY 240 NNLFGRSALKTASBLIAKENLKTSGSEVGAVNFFLVTALQAKAFLLTTCKRLGLAD 299
DB 241 NNLFGRSALKTASBLIAKENLKTSGSEVGAVNFFLVTALQAKAFLLTTCKRLGLAD 300
QY 300 IYTPIMNEHLNKEKEEFPNVNLLPTLSNTPSNPNYKARAGSDKAKIIMEAKPGYALVGF 359
DB 301 IYTPIMNEHLNKEKEEFPNVNLLPTLSNTPSNPNYKARAGSDKAKIIMEAKPGYALVGF 360
QY 360 EISKOSIAYLKYYOAKLKHNOQIDKOSISEIYVGIDILCLPDQSEQMYTNTKIAFPNEY 419
DB 361 EISKOSIAYLKYYOAKLKHNOQIDKOSISEIYVGIDILCLPDQSEQMYTNTKIAFPNEY 420
QY 420 VITKIAFTKQNSLREYVLANFYDSSTGDIIDLNKKKIESSEABFSMLNANDGVYMPIGT 479
DB 421 VITKIDFTKQKMTLREYVLANFYDSSTGDIIDLNKKKIESSEABFSMLNANDGVYMPIGT 480
QY 480 ISETFLTPINGGLVVDENSRLLVTLTCKSYLRETLATDLSNKETKLIIPPNGFISNIYE 539
DB 481 ISETFLTPINGGLVVDENSRLLVTLTCKSYLRETLATDLSNKETKLIIPPNGFISNIYE 540
QY 540 NGNLEGENLEFPWKANNKAYVDHTGVNGTGYLVYHEDGEPGQFIDKAKLKTREYVIOYT 599
DB 541 NGNLEGENLEFPWKANNKAYVDHTGVNGTGYLVYHEDGEPGQFIDKAKLKTREYVIOYT 600
QY 600 VKGKAALYLDKDEKNDYIYEETNNLEDFQAVTKKPFITGTSSRYHLIFTSONGEBAFG 659
DB 601 VKGKSIHLKDEKNTGYIHYEDTNNLEDFQAVTKKPFITGTDLKGYVLLKSGQGBEAMGD 660
QY 660 NFIISEIRPSEELSPBLIKSDAWGSGQTIWISGNSLINSVNGTFRONTLSLESYSTYS 719
DB 661 NFIISEIRPSEELSPBLIKSDAWGSGQTIWISGNSLINSVNGTFRONTLSLESYSTYS 720
QY 720 MNFVNGFGKTYTINSREVFERSYLOPSSKYISEKFTTTNTNGLYELSPASS--RG 776
DB 721 VYFVSVDANVIRINSREVLFEKRYMS-GAKDVSEMFYTKPEKONFYIELSGNNLYGCP 779
QY 777 VINFGDPSIK 786
DB 780 IVHFYDVSIK 789

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RESULT 8
045792_BACTU

ID Q45792_BACTU PRELIMINARY; PRT; 789 AA.
AC Q45792;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Vlp3A(A) protein.
GN Name=Vlp3A(a);
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1428;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AB88;
RX MEDLINE=96224295; PubMed=6643585; DOI=10.1073/pnas.93.11.5389;
RA Eertruch J.J., Warren G.W., Mullins M.A., Nye G.J., Craig J.A.,
RA Koziel M.G.;
RT "Vlp3A, a novel Bacillus thuringiensis vegetative insecticidal protein
RT with a wide spectrum of activities against lepidopteran insects.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:5389-5394(1996).
DR EMBL; I48811; AAC37036.1; -; Genomic DNA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR InterPro; IPR003305; CBM_Cenc.
DR Pfam; PF02018; CBM_4_9; 1.
DR Oxidoreductase.
SQ SEQUENCE 789 AA; 88671 MW; 9DD3DD926823C7AE CRC64;

Query Match 79.4%; Score 3171.5; DB 2; Length 789;
Best Local Similarity 78.5%; Pred. No. 2.8e-140;
Matches 620; Conservative 71; Mismatches 94; Indels 5; Gaps 3;

QY 1 MOKNN-KLSYKALPSFDYFNGIYGFATGIDIMNMIFKNTGDDLTLDELTKNQQLINE 59
DB 1 MNKNKNTLSRALPSFDYFNGIYGFATGIDIMNMIFKNTGDDLTLDELTKNQQLINE 60
QY 60 ISGKLDGVNSGLDLAQGNLDLSTKIKIANEQKVTNDVTKDAINMLNTYLPK 119
DB 61 ISGKLDGVNSGLDLAQGNLDLSTKIKIANEQKVTNDVTKDAINMLNTYLPK 120
QY 120 ITSMLSVDMKONVALGQIEYLSKQKEISDKLDVINNVNLINSTLEIFPAVORIKYVN 179
DB 121 ITSMLSVDMKONVALGQIEYLSKQKEISDKLDVINNVNLINSTLEIFPAVORIKYVN 180
QY 180 EKFEALTSATEPNTKTKODSSHTDILDELTELTELAKSVTKNDVGEFFYNTFHDWVG 239
DB 181 EKFEALTSATEPNTKTKODSSHTDILDELTELTELAKSVTKNDVGEFFYNTFHDWVG 240
QY 240 NNLFGRSALKTASSELIAKENIKTSGEVGNVYVFLVITLQAKAFLLTTCRKLGIAD 299
DB 241 NNLFGRSALKTASSELIAKENIKTSGEVGNVYVFLVITLQAKAFLLTTCRKLGIAD 300
QY 300 IDYPIPNNEHLNKKKEEPRVUILPLTSFTSPNPKYKRGSDKAKIIMEAKPGVALYGF 359
DB 301 IDYPIPNNEHLNKKKEEPRVUILPLTSFTSPNPKYKRGSDKAKIIMEAKPGVALYGF 360
QY 360 EISKDSIAVLKYVQAKLKHNYQIDKDSLSEIYVGDIDLCPDQSEQMYTNTKIAFPNEY 419
DB 361 EISKDSIAVLKYVQAKLKHNYQIDKDSLSEIYVGDIDLCPDQSEQMYTNTKIAFPNEY 420
QY 420 VITKIAFLPKLNSLREYVYANFYDSSTGDIIDLNKKKISSSAEFSMLNANDGYMPTGT 479
DB 421 VITKIAFLPKLNSLREYVYANFYDSSTGDIIDLNKKKISSSAEFSMLNANDGYMPTGT 480
QY 480 ISEFLPFLPFGGLVVDENSRLLVLTCKSYLRETLTLDLSNKKETKLVPPNGFISNIVE 539
DB 481 ISEFLPFLPFGGLVVDENSRLLVLTCKSYLRETLTLDLSNKKETKLVPPNGFISNIVE 540
QY 540 NGNLEGENLEBPWKANNKNAAYVDHTGVNGTFLVYVHEDEFSQFIDGKLKLTETEVLYQYI 599
DB 541 NGNLEGENLEBPWKANNKNAAYVDHTGVNGTFLVYVHEDEFSQFIDGKLKLTETEVLYQYI 600
QY 600 VKGKAALYLDKPKGVDYIEETNNELEDFQAVTKRFTTGDSRVHLIFTSQNGBEAFGG 659
DB 600 VKGKAALYLDKPKGVDYIEETNNELEDFQAVTKRFTTGDSRVHLIFTSQNGBEAFGG 659

DB 601 VKGKPSIHLKDENTGYIHYEDTNNNLEDYQINKRFTTGDLKGVYLKKSQNGDEAMGD 660
QY 660 NFITSEIRPSELSPELIKSDAMVSGQTWISGNSLINSNVNGFRONLSIESYSTYS 719
DB 661 NFITSEIRPSELSPELIKSDAMVSGQTWISGNSLINSNVNGFRONLSIESYSTYS 720
QY 720 MNFVNGFGVYIIRNSREVVFRSXYLOFSSKYSISEKFTTNTNGLVYELSRSS--RG 776
DB 721 VYFVSGDAMVRIIRNSREVVFEKRYMS-GAKDVSEMTTTFEKNPFYIELSQGNLYGCP 779
QY 777 VINFGDPSIK 786
DB 780 VYFVYVSIX 789

RESULT 9

ID Q8RS25_BACTU PRELIMINARY; PRT; 789 AA.
AC Q8RS25;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 10-MAY-2005 (Tremblrel. 30, Last annotation update)
DE Vlp3A (Vlp184).
GN Name=Vlp3A;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1428;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=5184;
RX MEDLINE=22744951; PubMed=12859763;
RX DOI=10.1046/j.1365-2672.2003.01977.x;
RA Chen J., Yu J., Tang L., Tang M., Shi Y., Pang Y.;
RT "Cloning and expression product of vlp3A gene from Bacillus
RT thuringiensis and analysis of insecticidal activity.";
RL Sheng Wu Gong Cheng Xue Bao 18:687-692(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=5184;
RX PubMed=12674638;
RA Chen J.W., Tang L.X., Tang M.J., Shi Y.X., Pang Y.;
RT "Cloning and expression product of vlp3A gene from Bacillus
RT thuringiensis and analysis of insecticidal activity.";
RL Sheng Wu Gong Cheng Xue Bao 18:687-692(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Chen J., Yu J., Pang Y.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY074706; AAL69542.1; -; Genomic DNA.
DR EMBL; AY187679; AAO32350.1; -; Genomic DNA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR InterPro; IPR003305; CBM_Cenc.
DR Pfam; PF02018; CBM_4_9; 1.
DR Oxidoreductase.
SQ SEQUENCE 789 AA; 88645 MW; D9DF334011551472 CRC64;

Query Match 79.4%; Score 3171.5; DB 2; Length 789;
Best Local Similarity 78.6%; Pred. No. 2.8e-140;
Matches 621; Conservative 69; Mismatches 95; Indels 5; Gaps 3;

QY 1 MOKNN-KLSYKALPSFDYFNGIYGFATGIDIMNMIFKNTGDDLTLDELTKNQQLINE 59
DB 1 MNKNKNTLSRALPSFDYFNGIYGFATGIDIMNMIFKNTGDDLTLDELTKNQQLINE 60
QY 60 ISGKLDGVNSGLDLAQGNLDLSTKIKIANEQKVTNDVTKDAINMLNTYLPK 119
DB 61 ISGKLDGVNSGLDLAQGNLDLSTKIKIANEQKVTNDVTKDAINMLNTYLPK 120
QY 120 ITSMLSVDMKONVALGQIEYLSKQKEISDKLDVINNVNLINSTLEIFPAVORIKYVN 179
DB 121 ITSMLSVDMKONVALGQIEYLSKQKEISDKLDVINNVNLINSTLEIFPAVORIKYVN 180

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QY 180 EKFEALTSATEFNLTAKODSSHTDILDELTELTELAKSVTKNDVDGFEFYLTNTHDWMIG 239
DB 181 EKFEELTFAETETSSKVKDQSPADILDELTELTELAKSVTKNDVDGFEFYLTNTHDWMIG 240
QY 240 NNLFGSALKTASELJAKENLKTSGSEGVNPNFLIVTLAQAKAFLLTTCRKLGLAD 299
DB 241 NNLFGSALKTASELJAKENLKTSGSEGVNPNFLIVTLAQAKAFLLTTCRKLGLAD 300
QY 300 IDYTPIMNEHLNKEKEEFRRVNIPLTSLNTPSNPNYKARGSDKAKIMEAKGYALVGF 359
DB 301 IDYTSIMNEHLNKEKEEFRRVNIPLTSLNTPSNPNYKARGSDKAKIMEAKGYALVGF 360
QY 360 EISKDSIAVLKYQAQAKNAYDHTGNGVNGTKVLYVHEDGFSGOFTGDKLKTVEVYIQT 419
DB 361 EISNDSITVLKYEAQAKNAYDHTGNGVNGTKVLYVHEDGFSGOFTGDKLKTVEVYIQT 420
QY 420 VTTKIAFTKCLNSLRVEYANFPYDSGTGIDLNKKKISSSEAFSMLNANDGVMPYIGT 479
DB 421 VTTKIDFTKCMKTLAREYANFPYDSGTGIDLNKKKISSSEAFSMLNANDGVMPYIGT 480
QY 480 ISETFLTPINGFGLVVDENSRLVTLTCKSYLRETLATDLNKKETKLIYPPNGFISNIVE 539
DB 481 ISETFLTPINGFGLVVDENSRLVTLTCKSYLRETLATDLNKKETKLIYPPNGFISNIVE 540
QY 540 NNLFGSALKTASELJAKENLKTSGSEGVNPNFLIVTLAQAKAFLLTTCRKLGLAD 299
DB 541 NNLFGSALKTASELJAKENLKTSGSEGVNPNFLIVTLAQAKAFLLTTCRKLGLAD 300
QY 300 IDYTPIMNEHLNKEKEEFRRVNIPLTSLNTPSNPNYKARGSDKAKIMEAKGYALVGF 359
DB 301 IDYTSIMNEHLNKEKEEFRRVNIPLTSLNTPSNPNYKARGSDKAKIMEAKGYALVGF 360
QY 600 VKGKAATYLDKDKNGDYIEETNNLEBDFOAVTKRFTGTDSRVHLITFSONGEAFGG 659
DB 601 VKGKPSIHLKDKNGDYIEETNNLEBDFOAVTKRFTGTDSRVHLITFSONGEAFGG 660
QY 660 NFIIEIRPSELLSPELIKSDAWVSGGTWISGNSLINSVNGTFRONTLSLSYSTYS 719
DB 661 NFIIEIRPSELLSPELIKSDAWVSGGTWISGNSLINSVNGTFRONTLSLSYSTYS 720
QY 720 MNFVNGFGKVTIRNSREVPERSYLOPSSKYISEKFTTTNNNGLYVHESRASS---RG 776
DB 721 VYFSVSGDANVRIRNSREVLFEKRYMS--GADVSEMTTKEKONFYIELSGNNLYGCP 779
QY 777 VINFGDFSIK 786
DB 780 IVHFYDVSIRK 789

RESULT 10
069270_BACTU
ID 069270_BACTU PRELIMINARY; PRT; 789 AA.
AC 069270;
DT 01-AUG-1998 (Tremblrel. 07, Created)
DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DB Vegetative insecticidal protein.
GN Name=vip-8;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OC NCBI_TaxID=1428;
RX MEDLINE=21579339; PubMed=11722946;
RA Selvapandian A., Arora N., Rajagopal R., Jalali S.K., Venkatesan T.,
Singh S.P., Bhattacharjee R.K.,
"toxicity analysis of N- and C-terminus-deleted vegetative
insecticidal protein from Bacillus thuringiensis.",
RL Appl. Environ. Microbiol. 67:5855-5858(2001).
DR EMBL: Y17158; CA76655.1; -; Genomic DNA.
DR GO: GO:0016491; P:oxidoreductase activity; IEA.
DR InterPro: IPR003305; CMB_Cenc.
DR Pfam: PF02018; CMB_4_9; I.
KW Oxidoreductase.

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SQ SEQUENCE 789 AA; 88539 MW; 70619EA86823C7AC CRC64;
Query Match 79.3%; Score 3168.5; DB 2; Length 789;
Best Local Similarity 78.5%; Pred. No.3.9e-140;
Matches 620; Conservative 70; Mismatches 95; Indels 5; Gaps 3;

QY 1 MOKNN-KLSVKAAPFIDYFNIGYFATGICIKIMNIPFTNTGGLTDEILKNOOLLNE 59
DB 1 MOKNTKSTRALPSPFIDYFNIGYFATGICIKIMNIPFTNTGGLTDEILKNOOLLNE 60
QY 60 ISGKLDGVNGSLINDLLAQNLDTELSEKILKIANBQNVKLVNDVTKDALINMLNTYLPK 119
DB 61 ISGKLDGVNGSLINDLLAQNLDTELSEKILKIANBQNVKLVNDVTKDALINMLNTYLPK 120
QY 120 ITSMISDVWKNYALGLQIEYISKQKESDGLDVYINNVVLIINSTLETTPAYOKIKYVN 179
DB 121 ITSMISDVWKNYALGLQIEYISKQKESDGLDVYINNVVLIINSTLETTPAYOKIKYVN 180
QY 180 EKFEALTSATEFNLTAKODSSHTDILDELTELTELAKSVTKNDVDGFEFYLTNTHDWMIG 239
DB 181 EKFEELTFAETETSSKVKDQSPADILDELTELTELAKSVTKNDVDGFEFYLTNTHDWMIG 240
QY 240 NNLFGSALKTASELJAKENLKTSGSEGVNPNFLIVTLAQAKAFLLTTCRKLGLAD 299
DB 241 NNLFGSALKTASELJAKENLKTSGSEGVNPNFLIVTLAQAKAFLLTTCRKLGLAD 300
QY 300 IDYTPIMNEHLNKEKEEFRRVNIPLTSLNTPSNPNYKARGSDKAKIMEAKGYALVGF 359
DB 301 IDYTSIMNEHLNKEKEEFRRVNIPLTSLNTPSNPNYKARGSDKAKIMEAKGYALVGF 360
QY 360 EISKDSIAVLKYQAQAKNAYDHTGNGVNGTKVLYVHEDGFSGOFTGDKLKTVEVYIQT 419
DB 361 EISNDSITVLKYEAQAKNAYDHTGNGVNGTKVLYVHEDGFSGOFTGDKLKTVEVYIQT 420
QY 420 VTTKIAFTKCLNSLRVEYANFPYDSGTGIDLNKKKISSSEAFSMLNANDGVMPYIGT 479
DB 421 VTTKIDFTKCMKTLAREYANFPYDSGTGIDLNKKKISSSEAFSMLNANDGVMPYIGT 480
QY 480 ISETFLTPINGFGLVVDENSRLVTLTCKSYLRETLATDLNKKETKLIYPPNGFISNIVE 539
DB 481 ISETFLTPINGFGLVVDENSRLVTLTCKSYLRETLATDLNKKETKLIYPPNGFISNIVE 540
QY 540 NNLFGSALKTASELJAKENLKTSGSEGVNPNFLIVTLAQAKAFLLTTCRKLGLAD 299
DB 541 NNLFGSALKTASELJAKENLKTSGSEGVNPNFLIVTLAQAKAFLLTTCRKLGLAD 300
QY 300 IDYTPIMNEHLNKEKEEFRRVNIPLTSLNTPSNPNYKARGSDKAKIMEAKGYALVGF 359
DB 301 IDYTSIMNEHLNKEKEEFRRVNIPLTSLNTPSNPNYKARGSDKAKIMEAKGYALVGF 360
QY 600 VKGKAATYLDKDKNGDYIEETNNLEBDFOAVTKRFTGTDSRVHLITFSONGEAFGG 659
DB 601 VKGKPSIHLKDKNGDYIEETNNLEBDFOAVTKRFTGTDSRVHLITFSONGEAFGG 660
QY 660 NFIIEIRPSELLSPELIKSDAWVSGGTWISGNSLINSVNGTFRONTLSLSYSTYS 719
DB 661 NFIIEIRPSELLSPELIKSDAWVSGGTWISGNSLINSVNGTFRONTLSLSYSTYS 720
QY 720 MNFVNGFGKVTIRNSREVPERSYLOPSSKYISEKFTTTNNNGLYVHESRASS---RG 776
DB 721 VYFSVSGDANVRIRNSREVLFEKRYMS--GADVSEMTTKEKONFYIELSGNNLYGCP 779
QY 777 VINFGDFSIK 786
DB 780 IVHFYDVSIRK 789

RESULT 11
04VYTO_BACTU
ID 04VYTO_BACTU PRELIMINARY; PRT; 789 AA.
AC 04VYTO;
DT 13-SEP-2005 (Tremblrel. 31, Created)
DT 13-SEP-2005 (Tremblrel. 31, Last sequence update)
DT 13-SEP-2005 (Tremblrel. 31, Last annotation update)
DB Vegetative insecticidal protein.
GN Name=vip3a;
OS Bacillus thuringiensis.

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OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1428;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BTAB51;
RA Pham N.B., Le N.H., Pham T.T., Chu H.H., Le B.T.;
RT "Cloning and sequence analysis gene encoding the vegetative
RT insecticidal protein (VIP3a) of some Vietnamese B. thuringiensis
RT strains." (May-2005) to the EMBL/GenBank/DBJ databases.
RL Submitted (May-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ971413; CAI96522.1; -; Genomic_DNA.
DR InterPro; IPR003305; Cenc Carb_bd.
DR Pfam; PF02018; CBM_4_9; 1.
KM Oxidoreductase.
SQ SEQUENCE 789 AA; 88614 MW; 5F255A098B9C86DD CRC64;

Query Match 79.3%; Score 3168.5; DB 2; Length 789;
Best Local Similarity 78.5%; Pred. No. 3.9e-140;
Matches 620; Conservative 70; Mismatches 95; Indels 5; Gaps 3;

QY 1 MOKNN-KLSVKAALPSFIDYFNGIYGATGIDIMNMIFKTNMGDLTLDLILKNOQLNE 59
DB 1 MNKNNTKLSRALPSFIDYFNGIYGATGIDIMNMIFKTDGDLTLDLILKNOQLNE 60
QY 60 ISGLDGVNGSLNDLLAQGNLDTELSEIKLKIANEQNVLDVNTKLDALNMLNTYLPK 119
DB 61 ISGLDGVNGSLNDLLAQGNLDTELSEIKLKIANEQNVLDVNTKLDALNMLNTYLPK 120
QY 120 ITSMLSVDMKQNYALGQIEYLSKQLEISDKLDVINNVNLINSTLEITPAYORIKYVN 179
DB 121 ITSMLSVDMKQNYALGQIEYLSKQLEISDKLDVINNVNLINSTLEITPAYORIKYVN 180
QY 180 EKPEALTSATETNLTAKDSSHTDILDELTELAKSVTKNDVGFEEFYNTFHDVWG 239
DB 181 EKPEALTSATETSSKVKKQSPADILDELTELAKSVTKNDVGFEEFYNTFHDVWG 240
QY 240 NNLFGRSALKTASSELIAKENLKTSGSEVGNVYNFLIVTLAQAKAFLLTTCRKLGLAD 299
DB 241 NNLFGRSALKTASSELITKENKTSSEVGNVYNFLIVTLAQAKAFLLTTCRKLGLAD 300
QY 300 IDYTPINMHLNKEKEEFRVNIPLTSLNTSPNPKYKARSGSDKAKIIMEAKPGYALVGF 359
DB 301 IDYTSIMNHLNKEKEEFRVNIPLTSLNTSPNPKYKARSGSDKAKIIMEAKPGHALIGF 360
QY 360 EISDSIAVLKQYQAKLKHNYQIDKDSLSEIVYGDIDKLCPPDSEQMYTNNKIAFPNEY 419
DB 361 EISDSITVLKQYKAKQNYQVDDSLSEVIYGDMDKLCPPDSEQMYTNNKIAFPNEY 420
QY 420 VITKIAFTKGLNSLRYEVTANFYDSTGDI DLNKKKISSSEAEFSMLNANNNGVYMPIGT 479
DB 421 VITKIDPTKOKTKRLRYEVTANFYDSTGDI DLNKKKISSSEAEFSMLNANNNGVYMPIGT 480
QY 480 ISEFTFLPINFGLVVDNSRLVTLTCKSYLRETLATDLSNKETKLI VPPNGFISNIVE 539
DB 481 ISEFTFLPINFGLVVDNSRLVTLTCKSYLRETLATDLSNKETKLI VPPNGFISNIVE 540
QY 540 NGNLEGEULBPKANNKAAVYDHGCVNGTKVLYVHDEGFSQPIGDKLKTETVYIYI 599
DB 541 NGNLEGEULBPKANNKAAVYDHGCVNGTKVLYVHDEGFSQPIGDKLKTETVYIYI 600
QY 600 VKGKAALYLDKKNQDYIYEETNNELDFQAVTKRFITGDSRVHLIFTSONGEAEFGG 659
DB 601 VKGKPSIHLKDBENTGYIHEEDTNNLEBYQITNKRFTTGDTLKVYLLKLSQNGDEAMGD 660
QY 660 NFIISEIRPSEELLSPELIKSDAWYSGTWISGNSLINSNVNGTFPQNTSLBSYSTYS 719
DB 661 NFIISEIRPSEELLSPELIKSDAWYSGTWISGNSLINSNVNGTFPQNTSLBSYSTYS 720
QY 720 MNPNVNGGKTYTINSRVEVFRSRLQSSKYSISKFTTTNNNGLYLVELSRAS--RG 776
DB 721 VYFSVSGDANVIRNSREVLFEKRYMS-GADVDSMFTTKPEKONFYELISQGNMLYGP 779

QY 777 VINFGDSIK 786
DB 780 IVHFYDVSIK 789

RESULT 12
Q4U3F5_BACTU
ID Q4U3F5_BACTU PRELIMINARY; PRT; 789 AA.
AC Q4U3F5;
DC 13-SEP-2005 (Tremblrel. 31, Created)
DT 13-SEP-2005 (Tremblrel. 31, Last sequence update)
DT 13-SEP-2005 (Tremblrel. 31, Last annotation update)
DE Vegetative insecticidal protein.
GN Name=VIP3A;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1428;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=LS1;
RA Lu X., Hao H., Sun S., Zhu M., Du K., Li G.;
RT "Vegetative insecticidal protein gene vip3A-LS1 from Bacillus
RT thuringiensis strain LS1."
RL Submitted (Apr-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; DQ016968; AA941427.1; -; Genomic_DNA.
DR InterPro; IPR003305; Cenc Carb_bd.
DR Pfam; PF02018; CBM_4_9; 1.
KM Oxidoreductase.
SQ SEQUENCE 789 AA; 88574 MW; A82803275AFEC19C CRC64;

Query Match 79.2%; Score 3163.5; DB 2; Length 789;
Best Local Similarity 78.4%; Pred. No. 6.7e-140;
Matches 619; Conservative 71; Mismatches 95; Indels 5; Gaps 3;

QY 1 MOKNN-KLSVKAALPSFIDYFNGIYGATGIDIMNMIFKTNMGDLTLDLILKNOQLNE 59
DB 1 MNKNNTKLSRALPSFIDYFNGIYGATGIDIMNMIFKTDGDLTLDLILKNOQLNE 60
QY 60 ISGLDGVNGSLNDLLAQGNLDTELSEIKLKIANEQNVLDVNTKLDALNMLNTYLPK 119
DB 61 ISGLDGVNGSLNDLLAQGNLDTELSEIKLKIANEQNVLDVNTKLDALNMLNTYLPK 120
QY 120 ITSMLSVDMKQNYALGQIEYLSKQLEISDKLDVINNVNLINSTLEITPAYORIKYVN 179
DB 121 ITSMLSVDMKQNYALGQIEYLSKQLEISDKLDVINNVNLINSTLEITPAYORIKYVN 180
QY 180 EKPEALTSATETNLTAKDSSHTDILDELTELAKSVTKNDVGFEEFYNTFHDVWG 239
DB 181 EKPEALTSATETSSKVKKQSPADILDELTELAKSVTKNDVGFEEFYNTFHDVWG 240
QY 240 NNLFGRSALKTASSELIAKENLKTSGSEVGNVYNFLIVTLAQAKAFLLTTCRKLGLAD 299
DB 241 NNLFGRSALKTASSELITKENKTSSEVGNVYNFLIVTLAQAKAFLLTTCRKLGLAD 300
QY 300 IDYTPINMHLNKEKEEFRVNIPLTSLNTSPNPKYKARSGSDKAKIIMEAKPGYALVGF 359
DB 301 IDYTSIMNHLNKEKEEFRVNIPLTSLNTSPNPKYKARSGSDKAKIIMEAKPGHALIGF 360
QY 360 EISDSIAVLKQYQAKLKHNYQIDKDSLSEIVYGDIDKLCPPDSEQMYTNNKIAFPNEY 419
DB 361 EISDSITVLKQYKAKQNYQVDDSLSEVIYGDMDKLCPPDSEQMYTNNKIAFPNEY 420
QY 420 VITKIAFTKGLNSLRYEVTANFYDSTGDI DLNKKKISSSEAEFSMLNANNNGVYMPIGT 479
DB 421 VITKIDPTKOKTKRLRYEVTANFYDSTGDI DLNKKKISSSEAEFSMLNANNNGVYMPIGT 480
QY 480 ISEFTFLPINFGLVVDNSRLVTLTCKSYLRETLATDLSNKETKLI VPPNGFISNIVE 539
DB 481 ISEFTFLPINFGLVVDNSRLVTLTCKSHRETLATDLSNKETKLI VPPNGFISNIVE 540
QY 540 NGNLEGEULBPKANNKAAVYDHGCVNGTKVLYVHDEGFSQPIGDKLKTETVYIYI 599
DB 541 NGNLEGEULBPKANNKAAVYDHGCVNGTKVLYVHDEGFSQPIGDKLKTETVYIYI 600

Db 541 NSIEEDNLEPWKANKNAAYDHTGCVNGTKALVYHKDGGISQFIGDKLKPKTEVYIQYT 600
QY 600 VKGKAAYLKDEKNGDIYEETNNLEDFQAVTKRPTIGTDSRVHLFTSONGERAFGG 659
Db 601 VKGKASIFLKDEKNGDIYEETNNLEDFQAVTKRPTIGTDSRVHLFTSONGERAFGG 660
QY 660 NFIIEIRPSEBELSPBLIKSDAMVGSQGTWISGNSLINSNVNGTFRONTLSBSYSTYS 719
Db 661 NFIIEIRPSEBELSPBLIKSDAMVGSQGTWISGNSLINSNVNGTFRONTLSBSYSTYS 720
QY 720 MNPVNGRGKXTIRNSREVVERSTLQSSKXISEKFTTTTNTGTYELSRASG---RG 776
Db 721 VYFVSQGANVRIRNSREVLFEKRYMS-GAKOVSEMTTKFKPKDNFYIELSGNNLYGSP 779
QY 777 VINPQDFSIX 786
Db 780 IYHFYDVSIX 789

RESULT 13
Q5JZY9_BACTU PRELIMINARY; PRT; 786 AA.
ID Q5JZY9_BACTU PRELIMINARY; PRT; 786 AA.
AC Q5JZY9_ 10-MAY-2005 (TREMBLrel. 30, Created)
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
DE Isp3b protein.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1428;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Van Rie J., Arnaut G., Boers A., Damme N.;
RT "Genes encoding insecticidal secreted proteins from Bacillus thuringiensis."
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ872071; CAI43276.1; -; Genomic DNA.
DR GO; GO:0016798; F:hydrolyase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0005975; F:carbohydrate metabolism; IEA.
DR InterPro; IPR003305; CBM_CenC.
DR Pfam; PF02018; CBM_4_9; I.
KW Oxidoreductase.
SQ SEQUENCE 786 AA; 88997 MW; B67FD67CBA56A57 CRC64;

Query Match 79.1%; Score 3160; DB 2; Length 786;
Best Local Similarity 78.6%; Pred. No. 9, 7e-140;
Matches 619; Conservative 74; Mismatches 91; Indels 4; Gaps 3;

QY 1 MQKNN-KLSVKALPSFIDYFNGIYGFATGIDKIMMIRKMTGSLTDELILKNOQLNE 59
Db 1 MNNMNAKIMARLPSFIDYFNGIYGFATGIDKIMMIRKMTGSLTDELILKNOQLNE 60
QY 60 ISGLDGVNGSLNDLAAQGNLDELTELSEIKLIANKONKVLNDVNTKLDALNMLNTYLPK 119
Db 61 ISGLDGVNGSLNDLAAQGNLDELTELSEIKLIANKONKVLNDVNTKLDALNMLNTYLPK 120
QY 120 ITSMUSDVMKQNYALGQIEYLSKQKEISDKLDVINNVNLINSTLTETPAYQRKTYN 179
Db 121 ITSMUSDVMKQNYALGQIEYLSKQKEISDKLDVINNVNLINSTLTETPAYQRKTYN 180
QY 180 EKPELTSATETNLTAKDSSHTDILDELTELSEIKLIANKONKVLNDVNTKLDALNMLNTYLPK 239
Db 181 EKPELTSATETNLTAKDSSHTDILDELTELSEIKLIANKONKVLNDVNTKLDALNMLNTYLPK 240
QY 240 NNLFGRSALKTASSELIAKENLTSSEYGVNYPFLIYVLTALQAKAFLLTTCRKLLGLAD 299
Db 241 NNLFGRSALKTASSELIAKENLTSSEYGVNYPFLIYVLTALQAKAFLLTTCRKLLGLAD 300
QY 300 IDYPIPMNEHLNKEKEEFRRVNLPLTSLNTFSNPYKARGSDKAKIIMEAKPGVALVGF 359
Db 301 IDYPIPMNEHLNKEKEEFRRVNLPLTSLNTFSNPYKARGSDKAKIIMEAKPGVALVGF 360

QY 360 BISKDSIAVLKYYQAKLKHNYQIDKDSLSEIYVGDIDKLCPDQSEOMYTTKIAFPNEY 419
Db 361 EMSNDSITVLKAYQAKLKHNYQIDKDSLSEIYVGDIDKLCPDQSEOMYTTKIAFPNEY 420
QY 420 VITKIAFTKQNSLREYVYANFYDSSTGIDILNKKKISSSEAFSMLNANDGVMPIGT 479
Db 421 VITKIAFTKQNSLREYVYANFYDSSTGIDILNKKKISSSEAFSMLNANDGVMPIGT 480
QY 480 ISETFLTPNGFGLVVDENSRVLTTCQSYARETLATDLSNKEKTKLIVPENGFSINVE 539
Db 481 ISETFLTPNGFGLVVDENSRVLTTCQSYARETLATDLSNKEKTKLIVPENGFSINVE 540
QY 540 NGNLEGENLEPWKANKNAAYDHTGCVNGTKVLYHHEGSESGQFGDKLKPKTEVYIQYT 599
Db 541 NGNLEGENLEPWKANKNAAYDHTGCVNGTKVLYHHEGSESGQFGDKLKPKTEVYIQYT 600
QY 600 VKGKAAYLKDEKNGDIYEETNNLEDFQAVTKRPTIGTDSRVHLFTSONGERAFGG 659
Db 601 VKGKASIFLKDEKNGDIYEETNNLEDFQAVTKRPTIGTDSRVHLFTSONGERAFGG 660
QY 660 NFIIEIRPSEBELSPBLIKSDAMVGSQGTWISGNSLINSNVNGTFRONTLSBSYSTYS 719
Db 661 NFIIEIRPSEBELSPBLIKSDAMVGSQGTWISGNSLINSNVNGTFRONTLSBSYSTYS 720
QY 720 MNPVNGRGKXTIRNSREVVERSTLQSSKXISEKFTTTTNTGTYELSRASG-VI 778
Db 721 VYFVSQGANVRIRNSREVLFEKRYL--NRGVSEMTTKFKPKDNFYIELSGNNLYGSP 779
QY 779 NFGDFSIX 786
Db 779 HFYDFSIX 786

RESULT 14
Q4U3F4_BACTU PRELIMINARY; PRT; 789 AA.
ID Q4U3F4_BACTU PRELIMINARY; PRT; 789 AA.
AC Q4U3F4_ 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE Vegetative insecticidal protein.
GN Name=vip3A;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1428;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lu X., Hao H., Sun S., Zhu M., Du K., Li G.;
RT "Vegetative insecticidal protein gene vip3A-Ls8 from Bacillus thuringiensis strain Ls8."
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; DQ016969; AA41428.1; -; Genomic_DNA.
DR InterPro; IPR003305; CenC_card_bd.
DR Pfam; PF02018; CBM_4_9; I.
KW Oxidoreductase.
SQ SEQUENCE 789 AA; 88540 MW; D4A09EDAA53898B3 CRC64;

Query Match 79.1%; Score 3159.5; DB 2; Length 789;
Best Local Similarity 78.2%; Pred. No. 1e-139;
Matches 618; Conservative 70; Mismatches 97; Indels 5; Gaps 3;

QY 1 MQKNN-KLSVKALPSFIDYFNGIYGFATGIDKIMMIRKMTGSLTDELILKNOQLNE 59
Db 1 MNNMNAKIMARLPSFIDYFNGIYGFATGIDKIMMIRKMTGSLTDELILKNOQLNE 60
QY 60 ISGLDGVNGSLNDLAAQGNLDELTELSEIKLIANKONKVLNDVNTKLDALNMLNTYLPK 119
Db 61 ISGLDGVNGSLNDLAAQGNLDELTELSEIKLIANKONKVLNDVNTKLDALNMLNTYLPK 120
QY 120 ITSMUSDVMKQNYALGQIEYLSKQKEISDKLDVINNVNLINSTLTETPAYQRKTYN 179

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 15, 2006, 20:43:31 ; Search time 47 Seconds
(without alignments)
1382.619 Million cell updates/sec

Title: US-10-698-096-17

Perfect score: 3395
Sequence: 1 MQKNKLSVKALPSFIDYFN.....VELSRASSRGVINFDEFSIK 786

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/1aa/5 COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/6 COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/H COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/PTUS COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/RE COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3505	87.7	787	2	US-09-307-106-54
2	3182.5	79.7	789	2	US-09-002-285-82
3	3182.5	79.7	789	2	US-09-589-477-82
4	3182.5	79.7	789	2	US-10-099-285A-82
5	3180.5	79.6	789	2	US-09-002-285-84
6	3180.5	79.6	789	2	US-09-589-477-84
7	3180.5	79.6	789	2	US-10-099-285A-84
8	3176.5	79.5	789	2	US-09-002-285-92
9	3176.5	79.5	789	2	US-09-589-477-92
10	3176.5	79.5	789	2	US-10-099-285A-92
11	3175.5	79.5	790	2	US-08-960-780-8
12	3175.5	79.5	790	2	US-09-073-898-8
13	3175.5	79.5	790	2	US-09-307-106-2
14	3175.5	79.5	790	2	US-09-850-351A-8
15	3171.5	79.4	789	2	US-08-471-033-29
16	3171.5	79.4	789	1	US-08-471-044-29
17	3171.5	79.4	789	1	US-08-463-483A-29
18	3171.5	79.4	789	1	US-08-471-046A-29
19	3171.5	79.4	789	1	US-08-470-566B-29
20	3171.5	79.4	789	1	US-08-838-219B-2
21	3171.5	79.4	789	1	US-08-469-334-29
22	3171.5	79.4	789	2	US-09-300-529-29
23	3171.5	79.4	789	2	US-09-233-336A-2
24	3171.5	79.4	789	2	US-09-233-336A-2
25	3171.5	79.4	789	2	US-09-402-036-2
26	3171.5	79.4	789	2	US-09-904-226-2
27	3170.5	79.4	789	2	US-09-002-285-78

28	3170.5	79.4	789	2	US-09-002-285-94	Sequence 94, Appl
29	3170.5	79.4	789	2	US-09-002-285-96	Sequence 96, Appl
30	3170.5	79.4	789	2	US-09-589-477-78	Sequence 78, Appl
31	3170.5	79.4	789	2	US-09-589-477-94	Sequence 94, Appl
32	3170.5	79.4	789	2	US-09-589-477-96	Sequence 96, Appl
33	3170.5	79.4	789	2	US-10-099-285A-78	Sequence 78, Appl
34	3170.5	79.4	789	2	US-10-099-285A-94	Sequence 94, Appl
35	3170.5	79.4	789	2	US-10-099-285A-96	Sequence 96, Appl
36	3167.5	79.3	789	2	US-08-960-780-6	Sequence 6, Appl
37	3167.5	79.3	789	2	US-09-073-898-6	Sequence 6, Appl
38	3167.5	79.3	789	2	US-09-850-351A-6	Sequence 6, Appl
39	3158.5	79.1	790	2	US-08-960-780-4	Sequence 4, Appl
40	3158.5	79.1	790	2	US-09-073-898-4	Sequence 4, Appl
41	3158.5	79.1	790	2	US-09-850-351A-4	Sequence 4, Appl
42	3156.5	79.0	789	1	US-08-471-033-32	Sequence 32, Appl
43	3156.5	79.0	789	1	US-08-471-044-32	Sequence 32, Appl
44	3156.5	79.0	789	1	US-08-463-483A-32	Sequence 32, Appl
45	3156.5	79.0	789	1	US-08-471-046A-32	Sequence 32, Appl

ALIGNMENTS

RESULT 1
US-09-307-106-54
Sequence 54, Application US/09307106
Patent No. 6603063
GENERAL INFORMATION:
APPLICANT: Fetteleson, Jerald S.
APPLICANT: Schieff, H. Ernest
APPLICANT: Narva, Kenneth B.
APPLICANT: Stockhoff, Brian A.
APPLICANT: Schneits, James
APPLICANT: Loewer, David
APPLICANT: Dullum, Charles Joseph
APPLICANT: Muller-Cohn, Judy
APPLICANT: Stamp, Lisa
APPLICANT: Morrill, George
APPLICANT: Pintad-Lee, Stacey
TITLE OF INVENTION: No. 6603063el Pesticidal Toxins and Nucleotide
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: US
ZIP: 32606-6669
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/307,106
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,848
FILING DATE: 30-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/960,780
FILING DATE: 30-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/073,898
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-708C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100

TELEFAX: 352-372-5800
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 787 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-307-106-54

Query Match 87.7%; Score 3505; DB 2; Length 787;
Best Local Similarity 87.1%; Pred. No. 1.5e-239;

Matches 682; Conservative 45; Mismatches 56; Indels 0; Gaps 0;

QY 4 NKKLSVAKLPSPFDYFNGIYGFATGIKDIMMIFKNTGSDLTDEILKNQQLNEISGK 63
DB 5 NTKLMARLPSPFDYFNGIYGFATGIKDIMMIFKNTGSDLTDEILKNQQLNEISGK 64
QY 64 LDGVNGSLNDLIAQGNLTLSKEILKIANEQNVLDVNNKLDALNTMLHIYLPKITSM 123
DB 65 LDGVNGSLNDLIAQGNLTLSKEILKIANEQNVLDVNNKLDALNTMLHIYLPKITSM 124
QY 124 LSDVMKQNYALGLQIEYLSKQLKEISDKDVINNVVLINSTLTETPAVQRIKYNKEPE 183
DB 125 LSDVMKQNYALSLQVEYLSKQLKEISDKDVINNVVLINSTLTETPAVQRIKYNKEPE 184
QY 184 ALTSATEINLKTDSSHTDILDELTELTELAKSVTKDNDVDFEFYNTFHDVWIGNNLF 243
DB 185 ELTFATETTLKVKKDSSPADILDELTELTELAKSVTKDNDVDFEFYNTFHDVWIGNNLF 244
QY 244 GRSLAKTASSELIAKENLKTSGSEGVGNVNFILVLTALQAKAFLLTTCRKILGLADIDYT 303
DB 245 GRSLAKTASSELIAKENLKTSGSEGVGNVNFILVLTALQAKAFLLTTCRKILGLADIDYT 304
QY 304 PIMNEHLNKKKEEPRVNIPLTSLNTFSPNPEYKARGSDKAKIMEAKPGVALVGEFISK 363
DB 305 SIMNEHLNKKKEEPRVNIPLTSLNTFSPNPEYKARGSDKAKIMEAKPGVALVGEFISK 364
QY 364 DSIAVLKLYQAKLKHNYQIDKDSLSEIYVGDIDQLCPDSEQWYTNKTLAPNEVYITK 423
DB 365 DSMTVLKLYBAKLKQNYQVDDKSLSEIYVSDMDQLCPDSEQWYTNKTLAPNEVYITK 424
QY 424 IAPTKLANSIRYEVTANFVDSSTGDDILANKKLESSAEFSMLNANDGVYMPIGTSET 483
DB 425 IDFTKQKTLRYEVTANFVDSSTGDDILANKKLESSAEFSMLNANDGVYMPIGTSET 484
QY 484 FLTPINGFGLVVENSLVTLTCKSYLRETLATLTDLSNKEKTLVPPNGFISINVENGNL 543
DB 485 FLTPINGFGLQADBNKSLITLTKCKSYLRETLATLTDLSNKEKTLVPPNGFISINVENGNL 544
QY 544 EGENLEBWKANNKQAVYDHTGVNGTKVLYVHEDGEFSPGIDKLKLTETEVYIQTIVKGR 603
DB 545 EGENLEBWKANNKQAVYDHTGVNGTKVLYVHEDGEFSPGIDKLKLTETEVYIQTIVKGR 604
QY 604 AATLYLDERKGDYIYETTNNELEDFOAVYTKFTTGDSSVHLIFTSQNGEBAPFGNFII 663
DB 605 AATLYLDERKGDYIYETTNNELEDFOAVYTKFTTGDSSVHLIFTSQNGEBAPFGNFII 664
QY 664 SEIRPSEBELLSPELISDAWVSGQTMISGNSLINSNVNCTPRONLSLESYTSYNNEN 723
DB 665 SEIRPSEBELLSPELISDAWVSGQTMISGNSLINSNVNCTPRONLSLESYTSYNNEN 724
QY 724 VNGFGKVTJNSREVEPERSYLOFSSKYLSEKFTYTTNNTGLVVELSRASSRGVINGDF 783
DB 725 VNGFGKVTJNSREVEPERSYLOFSSKYLSEKFTYTTNNTGLVVELSRASSRGVINGDF 784
QY 784 SIR 786
DB 785 SIR 787

RESULT 2
US-09-002-285-82

; Sequence 82, Application US/09002285
; Patent No. 6369213
; GENERAL INFORMATION:
; APPLICANT: Schneck, H. Ernest
; APPLICANT: Wicker, Carol
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Walz, Michelle
; APPLICANT: Stockhoff, Brian
; APPLICANT: Muller-Cohn, Judy
; TITLE OF INVENTION: Toxins Active Against Pests
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/002,285
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/886,615
; FILING DATE: 1-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/674,002
; FILING DATE: 1-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: MA-701C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 789 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-002-285-82

Query Match 79.7%; Score 3182.5; DB 2; Length 789;
Best Local Similarity 79.0%; Pred. No. 9.9e-217;

Matches 624; Conservative 69; Mismatches 92; Indels 5; Gaps 3;

QY 1 MQRNN-KLSVAKLPSPFDYFNGIYGFATGIKDIMMIFKNTGSDLTDEILKNQQLNE 59
DB 1 MNQNTKLSRALPSPFDYFNGIYGFATGIKDIMMIFKNTGSDLTDEILKNQQLNE 60
QY 60 ISGKLGVNGSLNDLIAQGNLTLSKEILKIANEQNVLDVNNKLDALNTMLHIYLPK 119
DB 61 ISGKLGVNGSLNDLIAQGNLTLSKEILKIANEQNVLDVNNKLDALNTMLHIYLPK 120
QY 120 ITSMISDWKQNYALGLQIEYLSKQLKEISDKDVINNVVLINSTLTETPAVQRIKYN 179
DB 121 ITSMISDWKQNYALSLQVEYLSKQLKEISDKDVINNVVLINSTLTETPAVQRIKYN 180
QY 180 EKREALTSATEINLKTDSSHTDILDELTELTELAKSVTKDNDVDFEFYNTFHDVMTG 239
DB 181 EKFEELTFATETTLKVKKDSSPADILDELTELTELAKSVTKDNDVDFEFYNTFHDVMTG 240
QY 240 NNLFGRSALKTASSELIAKENLKTSGSEGVGNVNFILVLTALQAKAFLLTTCRKILGLAD 299
DB 241 NNLFGRSALKTASSELIAKENLKTSGSEGVGNVNFILVLTALQAKAFLLTTCRKILGLAD 300

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QY 300 IDYTPINNEHLNKEKEFRVNIILPTLSNTPSNPYEKARSGDKAKIIMEAKPGYALVGF 359
D 301 IDYTSINNEHLNKEKEFRVNIILPTLSNTPSNPYAKVKSDEDEKMIIVEAKPGYALVGF 360
QY 360 EISKDSIAVLKQYQAKLKHNTQIDKOSLSIYVGDIDKLCPODSEQMYTNNKIAFPNEY 419
D 361 EMSNDSITVLKYVEBAKQKONYQVOKDSISEVIYGDIDKLCPODSEQIYYTNNIIVFPNEY 420
QY 420 VITKIAFTKRLNSRYEVTANFYDSSGTGIDLNKKKIESSEAEPSMANNNDGYMPTIGT 479
D 421 VITKIDFTKRMKTLRYEVTANFYDSSGTGIDLNKKKVESSEAEPRITLSANDGVYMPILGV 480
QY 480 ISETFLTPINGFGLVVDENSRVLTLCKSYLRETLATDLSNKEKLIIVPNGFISNIIVE 539
D 481 ISETFLTPINGFGLQADGNSRLITLTKSYLRELLATDLSNKEKLIIVPSPGISNIIVE 540
QY 540 NGNLEGERLEPWKANNKAAVYDHTGVNGTVLYVHEDGEFSQFIGDKLKTEYVIQYI 599
D 541 NGSIEEDNLBPWKANNKAAVYDHTGVNGTKALYVHKDGFSGFIGDKLKTEYVIQYT 600
QY 600 VKGAATYILKDEKQNDYIYEETNNELEDPOAVTKRFTIGDSSRVHLIFTSONGEBAFG 659
D 601 VKGPSIHLKDEKNTGYIHYBDNNNLKDYQITTKRFTTGIDLKGVYLLKSGNGDEAWGD 660
QY 660 NFIISEIRPSEELLSPBLIKSDAWVSGQWTWISGNSLINSNVNGTFRQNLLESYSTYS 719
D 661 NFIILEISPSSEKLSPELIINTNMSTGTHISGNTLTLVYOGRGILKQULDSFSTYR 720
QY 720 MNFNVNGKQVTTIRNSREVEFSYLOPSSKYISEKFTTTNNGLYVELSRASS---RG 776
D 721 VYFVSQGANVRIIRNSREVLFEKRYMS-GAKDVSEMFTEKFEKONFYIELSQNNLVYGGP 779
QY 777 VINFGDPSIK 786
D 780 IVHFNDSIK 789

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RESULT 3
US-09-589-477-82
Sequence 82, Application US/09589477
Patent No. 6570005
GENERAL INFORMATION:
APPLICANT: Schepf, H. Ernest
APPLICANT: Wicker, Carol
APPLICANT: Narva, Kenneth E.
APPLICANT: Walz, Michelle
APPLICANT: Stockhoff, Brian
TITLE OF INVENTION: Toxins Active Against Pests
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/589,477
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/886,615
FILING DATE: 1-JUL-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/674,002
FILING DATE: 1-JUL-1996
CLASSIFICATION:

```

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ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M. 39,355
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-701C1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 789 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-589-477-82

Query Match 79.7%; Score 3182.5; DB 2; Length 789;
Best Local Similarity 79.0%; Pred. No. 9,96-217;
Matches 624; Conservative 69; Mismatches 92; Indels 5; Gaps 3;

QY 1 MOKN-KLSYKALPSPIDYRNGIYGPATGIDIMNMIFKTNVGGDLTLDLILKQOOLINE 59
D 1 MNKNNTLSRTRALPSFDYFNGIYGPATGIDIMNMIFKTDVGGNLTLDLILKQOOLINE 60
QY 60 ISGLDGVNGLNDLDAQNLDPTELSKEILKIANEQKVLNDVNTKLDATNMAMTYLPK 119
D 61 ISGLDGVNGLNDLDAQNLDPTELSKEILKIANEQKVLNDVNTKLDATNMAMTYLPK 120
QY 120 ITSMLSVDMKQNVALGLQIEYLSKQLEISDKLDVINNVNLINSTLEITPAYORIKYVN 179
D 121 ITSMLSVDMKQNVALGLQIEYLSKQLEISDKLDVINNVNLINSTLEITPAYORIKYVN 180
QY 180 EKFEALTSAETBNKTKQDSSHTDIDELTELTBLAKSVTKNDVGEFEYLNTEFHDVIG 239
D 181 EKFEALTSAETBNKTKQDSSHTDIDELTELTBLAKSVTKNDVGEFEYLNTEFHDVIG 240
QY 240 NNLFGRSALKTASELAKENLKTSGSEVGNVNFVLYLTLOAKAFLTLTCRLGLAD 299
D 241 NNLFGRSALKTASELAKENLKTSGSEVGNVNFVLYLTLOAKAFLTLTCRLGLAD 300
QY 300 IDYTPINNEHLNKEKEFRVNIILPTLSNTPSNPYEKARSGDKAKIIMEAKPGYALVGF 359
D 301 IDYTSINNEHLNKEKEFRVNIILPTLSNTPSNPYAKVKSDEDEKMIIVEAKPGYALVGF 360
QY 360 EISKDSIAVLKQYQAKLKHNTQIDKOSLSIYVGDIDKLCPODSEQMYTNNKIAFPNEY 419
D 361 EMSNDSITVLKYVEBAKQKONYQVOKDSISEVIYGDIDKLCPODSEQIYYTNNIIVFPNEY 420
QY 420 VITKIAFTKRLNSRYEVTANFYDSSGTGIDLNKKKIESSEAEPSMANNNDGYMPTIGT 479
D 421 VITKIDFTKRMKTLRYEVTANFYDSSGTGIDLNKKKVESSEAEPRITLSANDGVYMPILGV 480
QY 480 ISETFLTPINGFGLVVDENSRVLTLCKSYLRETLATDLSNKEKLIIVPNGFISNIIVE 539
D 481 ISETFLTPINGFGLQADGNSRLITLTKSYLRELLATDLSNKEKLIIVPSPGISNIIVE 540
QY 540 NGNLEGERLEPWKANNKAAVYDHTGVNGTVLYVHEDGEFSQFIGDKLKTEYVIQYI 599
D 541 NGSIEEDNLBPWKANNKAAVYDHTGVNGTKALYVHKDGFSGFIGDKLKTEYVIQYT 600
QY 600 VKGAATYILKDEKQNDYIYEETNNELEDPOAVTKRFTIGDSSRVHLIFTSONGEBAFG 659
D 601 VKGPSIHLKDEKNTGYIHYBDNNNLKDYQITTKRFTTGIDLKGVYLLKSGNGDEAWGD 660
QY 660 NFIISEIRPSEELLSPBLIKSDAWVSGQWTWISGNSLINSNVNGTFRQNLLESYSTYS 719
D 661 NFIILEISPSSEKLSPELIINTNMSTGTHISGNTLTLVYOGRGILKQULDSFSTYR 720
QY 720 MNFNVNGKQVTTIRNSREVEFSYLOPSSKYISEKFTTTNNGLYVELSRASS---RG 776
D 721 VYFVSQGANVRIIRNSREVLFEKRYMS-GAKDVSEMFTEKFEKONFYIELSQNNLVYGGP 779
QY 777 VINFGDPSIK 786

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Db 61 ISGKLDGVNGSLNDLIAQGNINTELSEIKLIANEQOVINDVNNKLDAINTMLHIYLPK 120
QY 120 ITSMISDVWKQNYALGLQIEYLSKOLKEISDKLDIVNNVLIINSTLTETPAYORIKYVN 179
Db 121 ITSMISDVWKQNYALSLQIEYLSKOLKEISDKLDIIVNNVLIINSTLTETPAYORIKYVN 180
QY 180 EKFEALTSATETNLKTQDSSHTDILDELTELTELAKSVTKNDVDGFEFYLTFFHVMIG 239
Db 181 EKFEALTSATETNLKTQDSSHTDILDELTELTELAKSVTKNDVDGFEFYLTFFHVMIG 240
QY 240 NNLFGRSALKTASBLIAKENLKTSGSEVGNVNFILVLTALQAKAFILTTTCRKLGLAD 299
Db 241 NNLFGRSALKTASBLIAKENLKTSGSEVGNVNFILVLTALQAKAFILTTTCRKLGLAD 300
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Db 301 IDYTSIMNEHLNKEEKEFRVNIILPTLSNTFSNPYERKARSDKDAKIIMEAKGVALYGF 360
QY 360 EISKDSIAVLKYVQAKIKANYQIDKDSLSSEIVYGDIDKLLCPDQSEOMYTTNKIAFPNEY 419
Db 361 EWSNDSITVLKYBAKLKQNYOVDKSLSEIVYGDIDKLLCPDQSEQIYYTNNIVFPNEY 420
QY 420 VITKIAFTKLNLSRYEVTANFYDSSSTGDIIDLNKKKIESSEAFSMTNANDGVMPDGT 479
Db 421 VITKIDPTKQKTLRYEVIANFYDSSSTGDIIDLNKKKIESSEAFSMTNANDGVMPDGT 480
QY 480 ISETFLTPINGFGLVVDENSRLVLTCKSYLRETLATDLSNKEKTLVPPNGFISNIYE 539
Db 481 ISETFLTPINGFGLQADGNSRLITLTCKSYLRETLATDLSNKEKTLVPPNGFISNIYE 540
QY 540 NGNLEGENLEPWKANNKAAVYDHTGVNGTKVLYVHEDGFSQFIGDKLKLTETVYIOYI 599
Db 541 NGNLEGENLEPWKANNKAAVYDHTGVNGTKVLYVHEDGFSQFIGDKLKLTETVYIOYI 600
QY 600 VKSKAAILYKDEKNGDIYIETINNELEDFOAVTKRFTGDDSRVHLIFTSNGEERAFGG 659
Db 601 VKKPSIHLKDEMYTGIHEDTNNKLDVOTITKRFITGDLKGVYLLIKSQGDENWGD 660
QY 660 NFIIISIRPSEELLSPELIKSDAMVGSQGTWISGNSININSVNGTFRONLSIESYSTYS 719
Db 661 NFIIISIRPSEELLSPELINWNTSTGSHISGNLTLYQGRGILKQMLQDLSSTYR 720
QY 720 MNFNNGFGKVTIRNSREVVEFSYLOFSKYSISEKFTTTNTNGLYVELSRASS--RG 776
Db 721 VYFVSVDANVRIRNSREVLFEKGYS-CAKDVSEMTTKFEKONFYIELSQGNLNYGCG 779
QY 777 VINFGDSIK 786
Db 780 IYHFYVSIK 789

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RESULT 7
US-10-099-285A-84
; Sequence 84, Application us/10099285A
; Patent No. 6752992
; GENERAL INFORMATION:
; APPLICANT: Schmepl, H. Ernest
;           Wicker, Carol
;           Narva, Kenneth E.
;           Walz, Michelle
;           Stockhoff, Brian
;           Muller-Cohn, Judy
; TITLE OF INVENTION: Toxins Active Against Pests
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/099,285A
; FILING DATE: 02-Jul-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/002,285
; FILING DATE: 31-DEC-1997
; APPLICATION NUMBER: US 08/886,615
; FILING DATE: 1-JUL-1997
; APPLICATION NUMBER: US 08/674,002
; FILING DATE: 1-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: MA-701C2D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 789 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 84:
US-10-099-285A-84

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Query Match 79.6%; Score 3180.5; DB 2; Length 789;

Best Local Similarity 78.9%; Pred. No. 1,4e-216;

Matches 623; Conservative 70; Mismatches 92; Indels 5; Gaps 3;

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QY 1 MOKNN-KLSVKALPSFIDYFNGIYGFATGIKDIMNMIFFKNTGGLTDEILIKNOQLNE 59
Db 1 MNKNNTKLSARALPSFIDYFNGIYGFATGIKDIIMNMIFFKNTGGLTDEILIKNOQLNE 60
QY 60 ISGKLDGVNGSLNDLIAQGNINTELSEIKLIANEQOVINDVNNKLDAINTMLHIYLPK 119
Db 61 ISGKLDGVNGSLNDLIAQGNINTELSEIKLIANEQOVINDVNNKLDAINTMLHIYLPK 120
QY 120 ITSMISDVWKQNYALGLQIEYLSKOLKEISDKLDIVNNVLIINSTLTETPAYORIKYVN 179
Db 121 ITSMISDVWKQNYALSLQIEYLSKOLKEISDKLDIIVNNVLIINSTLTETPAYORIKYVN 180
QY 180 EKFEALTSATETNLKTQDSSHTDILDELTELTELAKSVTKNDVDGFEFYLTFFHVMIG 239
Db 181 EKFEALTSATETNLKTQDSSHTDILDELTELTELAKSVTKNDVDGFEFYLTFFHVMIG 240
QY 240 NNLFGRSALKTASBLIAKENLKTSGSEVGNVNFILVLTALQAKAFILTTTCRKLGLAD 299
Db 241 NNLFGRSALKTASBLIAKENLKTSGSEVGNVNFILVLTALQAKAFILTTTCRKLGLAD 300
QY 300 IDYTPIMNEHLNKEEKEFRVNIILPTLSNTFSNPYERKARSDKDAKIIMEAKGVALYGF 359
Db 301 IDYTSIMNEHLNKEEKEFRVNIILPTLSNTFSNPYERKARSDKDAKIIMEAKGVALYGF 360
QY 360 EISKDSIAVLKYVQAKIKANYQIDKDSLSSEIVYGDIDKLLCPDQSEOMYTTNKIAFPNEY 419
Db 361 EWSNDSITVLKYBAKLKQNYOVDKSLSEIVYGDIDKLLCPDQSEQIYYTNNIVFPNEY 420
QY 420 VITKIAFTKLNLSRYEVTANFYDSSSTGDIIDLNKKKIESSEAFSMTNANDGVMPDGT 479
Db 421 VITKIDPTKQKTLRYEVIANFYDSSSTGDIIDLNKKKIESSEAFSMTNANDGVMPDGT 480
QY 480 ISETFLTPINGFGLVVDENSRLVLTCKSYLRETLATDLSNKEKTLVPPNGFISNIYE 539
Db 481 ISETFLTPINGFGLQADGNSRLITLTCKSYLRETLATDLSNKEKTLVPPNGFISNIYE 540
QY 540 NGNLEGENLEPWKANNKAAVYDHTGVNGTKVLYVHEDGFSQFIGDKLKLTETVYIOYI 599

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Db 541 NGSEEDNLEBPWKANNNAAYVDHGTGVNGTKALVYHKDGFSPQIGDKLKEPTEYVIOYT 600
Qy 600 VKGAATYLDKDNKNDYIYEETNNLEDFQAVTKRFTINGTDSRVHILFTSONGEBAFG 659
Db 601 VKGPRSHLDKDNKNDYIYEDTNNNLKDYOTITKFTTGDKGVYLILKSQNGDEAMGD 660
Qy 660 NFIISEIRPSEBELLSPELIKSDAWVSGQWTWISGNSLNINSVNGTFRONLSLESTYS 719
Db 661 NFIILEISPSBKLSPELINTNNMTSTGTHISGNTLTLVQGGRIILKQNLQDLSFSTYR 720
Qy 720 MNFVNGFGKVTIRNSREVVFRSLOFSSKTISEKFTTTNNGLYVELSRASS--RG 776
Db 721 VYFVSVDANVRIRNSREVLFEKGYMS-GADVSEMFTTKEBKONFYIELSQGNLXYGP 779
Qy 777 VINFDFPSIK 786
Db 780 IVHFYDVSIX 789
RESULT 8
US-09-002-285-92
; Sequence 92, Application US/09002285
; Patent No. 6369213
; GENERAL INFORMATION:
; APPLICANT: Schnepf, H. Ernest
; APPLICANT: Wicker, Carol
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Walz, Michelle
; APPLICANT: Stochhoff, Brian
; APPLICANT: Muller-Cohn, Judy
; TITLE OF INVENTION: Toxins Active Against Pests
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/002,285
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/886,615
; FILING DATE: 1-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/674,002
; FILING DATE: 1-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: MA-701C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 789 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-002-285-92
Query Match 79.5%; Score 3176.5; DB 2; Length 789;
Best Local Similarity 78.9%; Pred. No. 2.6e-216;
Matches 623; Conservative 69; Mismatches 93; Indels 5; Gaps 3;

Qy 1 MOKAN-KLSVKALPSFIDYENGIVGPATGIDIMNMIKPTNTGGDLTLDEILKNQOOLNE 59
Db 1 MKNKNTKLSAPALBSFIDYENGIVGPATGIDIMNMIKPTDTGGNLTLDEILKNQOOLNE 60
Qy 60 ISGLDGVNGSLNDLQAQNLDELSEKILKIANEONKRVNDVTKDALINMLNLYLPK 119
Db 61 ISGLDGVNGSLNDLQAQNLDELSEKILKIANEONQVNDVNNKDALINMLNLYLPK 120
Qy 120 ITSMLSVDMKQNYALSLQIEYLSKQKEISPKULDIVINVTILNSTLREITPAORIKYV 179
Db 121 ITSMLSVDMKQNYALSLQIEYLSKQKEISPKULDIVINVTILNSTLREITPAORIKYV 180
Qy 180 EKFEALTSATEYNLKTQDSSHTDILDELTELTELASVTKNQDVGFEFYNTFHWVIG 239
Db 181 EKFEALTSATEYNLKTQDSSHTDILDELTELTELASVTKNQDVGFEFYNTFHWVIG 240
Qy 240 NNLFGRSALKTASELAKENLKTSGSEVGVNVELVLTALQAKAPLTLTTCRLGLAD 299
Db 241 NNLFGRSALKTASELAKENLKTSGSEVGVNVELVLTALQAKAPLTLTTCRLGLAD 300
Qy 300 IDYTPINMEHLNKEKEFRVNIILPTLNTSNNPYEAKGSDKAKIIMEAKPGYALVGF 359
Db 301 IDYTSINMEHLNKEKEFRVNIILPTLNTSNNPYEAKGSDKAKIIMEAKPGYALVGF 360
Qy 360 EISKDSIAYLKVYQAKLKHNYQIDKDSLSEIVYGDIKLCPDQSEOMYYTNKIAFPNEY 419
Db 361 EKSNDISITVLKVTAKLKNYQVNDKSLSEVYIGDTKLCPDQSEQYITNNIVFNEY 420
Qy 420 VITKIAFTKCLNSLREYVTAIFYDSSTGDIIDLNKKLESSEAEFSMLNANDGYMPLGT 479
Db 421 VITKIDFTKCKKTLREYVTAIFYDSSTGDIIDLNKKLESSEAEFSMLNANDGYMPLGV 480
Qy 480 ISEFTFLPPIGFGVLVDENSRVLVLTCKSYLRETLATDLSNKTGLVPPNGTISNVE 539
Db 481 ISEFTFLPPIGFGVLVDENSRVLVLTCKSYLRETLATDLSNKTGLVPPNGTISNVE 540
Qy 540 NGNLEGENLEBPWKANNNAAYVDHGTGVNGTKALVYHKDGFSPQIGDKLKEPTEYVIOYT 599
Db 541 NGSEEDNLEBPWKANNNAAYVDHGTGVNGTKALVYHKDGFSPQIGDKLKEPTEYVIOYT 600
Qy 600 VKGAATYLDKDNKNDYIYEETNNLEDFQAVTKRFTINGTDSRVHILFTSONGEBAFG 659
Db 601 VKGPRSHLDKDNKNDYIYEDTNNNLKDYOTITKFTTGDKGVYLILKSQNGDEAMGD 660
Qy 660 NFIISEIRPSEBELLSPELIKSDAWVSGQWTWISGNSLNINSVNGTFRONLSLESTYS 719
Db 661 NFIILEISPSBKLSPELINTNNMTSTGTHISGNTLTLVQGGRIILKQNLQDLSFSTYR 720
Qy 720 MNFVNGFGKVTIRNSREVVFRSLOFSSKTISEKFTTTNNGLYVELSRASS--RG 776
Db 721 VYFVSVDANVRIRNSREVLFEKGYMS-GADVSEMFTTKEBKONFYIELSQGNLXYGP 779
Qy 777 VINFDFPSIK 786
Db 780 IVHFYDVSIX 789
RESULT 9
US-09-589-477-92
; Sequence 92, Application US/09589477
; Patent No. 6570005
; GENERAL INFORMATION:
; APPLICANT: Schnepf, H. Ernest
; APPLICANT: Wicker, Carol
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Walz, Michelle
; APPLICANT: Stochhoff, Brian
; TITLE OF INVENTION: Toxins Active Against Pests
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/589,477
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/886,615
FILING DATE: 1-JUL-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/674,002
FILING DATE: 1-JUL-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-701C1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 92:
SEQUENCE CHARACTERISTICS:
LENGTH: 789 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-589-477-92

Query Match 79.5%; Score 3176.5; DB 2; length 789;
Best Local Similarity 78.9%; Pred. No. 2.6e-216;
Matches 623; Conservative 69; Mismatches 93; Indels 5; Gaps 3;

QY 1 MOKNN-KLSYKALPSFDYNGYIGPATGKIDMNMIFKNTGCDLTLDEILKNOOLANE 59
DB 1 MNKNNTKLSARALPSFDYNGYIGPATGKIDMNMIFKNTGCDLTLDEILKNOOLANE 60
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DB 61 ISGKLDGVNSLNDLLAOGNLDTLSKEIKIANEONKYNLVNTKLDATNMLNTYLPK 120
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QY 180 EKEEALTSANTENMLTKKODSHDIIIDELTELTELAKSVTKNDVDGFEPLNTFHDVWG 239
DB 181 EKEEALTSANTENMLTKKODSHDIIIDELTELTELAKSVTKNDVDGFEPLNTFHDVWG 240
QY 240 NNLFGSALKTASELTAKENLKTSGSEVGNVNFLLVLTALQAKAFLLTTCGLGLAD 299
DB 241 NNLFGSALKTASELTAKENLKTSGSEVGNVNFLLVLTALQAKAFLLTTCGLGLAD 300
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QY 360 EISKSDIATLKYQAQLKKNYQDKDLSLSEIVYGDIDKILCPQSQMTYNTKIAFPNEY 419
DB 361 EISKSDIATLKYQAQLKKNYQDKDLSLSEIVYGDIDKILCPQSQMTYNTKIAFPNEY 420
QY 420 VITKIAFTKILNSLREYEVANFYDSSTGDIIDLNKKKIESSEAFSLNANNNGVWVPIGT 479
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QY 480 ISETFLPINGFGLVNDENSLVTLFCKSYLRETLATLSDNKEKLIYVPPNGFISNIVE 539
DB 481 ISETFLPINGFGLVNDENSLVTLFCKSYLRETLATLSDNKEKLIYVPPNGFISNIVE 540
QY 540 NGNIEGENLEPMKANNKNAVYDHTGVNGTKVLYVHEDGFSQFIGDKLXKTEYVIOYI 599
DB 541 NGNIEGENLEPMKANNKNAVYDHTGVNGTKVLYVHEDGFSQFIGDKLXKTEYVIOYI 600
QY 600 VKGKAAYLKDEKNGDIYEETNNELEDPAVYKRPFTIGDSRVALIFTSQNGEAPFG 659
DB 601 VKGKAAYLKDEKNGDIYEETNNELEDPAVYKRPFTIGDSRVALIFTSQNGEAPFG 660
QY 660 NFIISERPEEELISPELLIKSDAMVGSQGTWISGNSLINSNVNGTFRONLSSEYSTYS 719
DB 661 NFIISERPEEELISPELLIKSDAMVGSQGTWISGNSLINSNVNGTFRONLSSEYSTYS 720
QY 720 MAFNVNPGKVTIRNSREVVERSYIQFSSKYSIEKFTTNTNGLYVELSRAS--RG 776
DB 721 VYFVSFGDANVIRNSREVVERSYIQFSSKYSIEKFTTNTNGLYVELSRAS--RG 777
QY 777 VINFGPESIK 786
DB 780 VYFVSFGDANVIRNSREVVERSYIQFSSKYSIEKFTTNTNGLYVELSRAS--RG 789

RESULT 10
US-10-099-285A-92
Sequence 92, Application US/10099285A
Patent No. 675292
GENERAL INFORMATION:
APPLICANT: Schuepf, H. Ernest
Wicker, Carol
Narva, Kenneth E.
Walz, Michelle
Stoekhoff, Brian
Muller-Cohn, Judy
TITLE OF INVENTION: Toxins Active Against Pests
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/099,285A
FILING DATE: 02-Jul-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/002,285
FILING DATE: 31-DEC-1997
APPLICATION NUMBER: US 08/886,615
FILING DATE: 1-JUL-1997
APPLICATION NUMBER: US 08/674,002
FILING DATE: 1-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-701C2D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 92:
SEQUENCE CHARACTERISTICS:
LENGTH: 789 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 92:
US-10-099-265A-92

Query Match 79.5%; Score 3176.5; DB 2; Length 789;
Best Local Similarity 78.9%; Pred. No. 2.6e-216;
Matches 623; Conservative 69; Mismatches 93; Indels 5; Gaps 3;

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QY 1 MOKNN-KLSYKALPSFIDYNGIYGFATGIDIMNMIKFTNTGGDLTLDELTKNOQLNE 59
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Db 1 MNKNNTKLSARALPSFIDYNGIYGFATGIDIMNMIKFTNTGGDLTLDELTKNOQLNE 60
QY 60 ISGLDGVNGSLNDLDAQNLDTLSKEIILKIANEQKVNDVNTKDAINMLNTYLPK 119
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 ISGLDGVNGSLNDLDAQNLDTLSKEIILKIANEQKVNDVNTKDAINMLNTYLPK 120
QY 120 ITSMUSDVMKONVALSIQIEYLSKQLEISDKLDVINNVNLINSTLEITPAYORIKYVN 179
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 ITSMUSDVMKONVALSIQIEYLSKQLEISDKLDVINNVNLINSTLEITPAYORIKYVN 180
QY 180 EKFEALTSATETNKTQDSSHTDIDDELTELTELAKSVTKNDVDGFEFYANTFHDVWG 239
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Db 181 EKFEALTSATETNKTQDSSHTDIDDELTELTELAKSVTKNDVDGFEFYANTFHDVWG 240
QY 240 NNLFGRSALKTASSELIAKENLKTSGSEVGVNPNFLIYLTALQAKAFLLTTCRKLGLAD 299
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Db 241 NNLFGRSALKTASSELIAKENLKTSGSEVGVNPNFLIYLTALQAKAFLLTTCRKLGLAD 300
QY 300 IDYTPINNEHLNKEKEEFVNILPTLSNTFSNPNYEKARSGDKAKIMEAKPGYALVGF 359
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QY 360 EISDQSLAVLKVYQAKLKNVQIDKDSISEIYVGDIDKLCPDQSEQMTYNNKAFPNEX 419
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 361 EMSNDSTIVLKVYAKKQNYQVDKDSISEVIYGDIDKLCPDQSEQMTYNNKAFPNEX 420
QY 420 VITKIAFTKQKLSIYREVTANFYDSGTGDIIDLNKKIIESSAEFSPMLNANDGYMPTGT 479
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 421 VITKIDFTKQKTIYREVTANFYDSGTGDIIDLNKKIIESSAEFSPMLNANDGYMPTGT 480
QY 480 ISEFTLTPINGFGLVVDENSHLVLTCKSYLRETLATLDSNKTCLVPPNGFISNIVE 539
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 481 ISEFTLTPINGFGLVVDENSHLVLTCKSYLRETLATLDSNKTCLVPPNGFISNIVE 540
QY 540 NGNLEGENLEBPWKANNKXAYVDHTGVNGYVLYVHEDGESQPIGDKLKXTEVYIQYI 599
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 541 NGNLEGENLEBPWKANNKXAYVDHTGVNGYVLYVHEDGESQPIGDKLKXTEVYIQYI 600
QY 600 VKGQALYLDQBNKGDYIYEETNNELEDPQAVTKRFTGTSSRVHLIFTSQNGEARGG 659
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 601 VKGQPSIHLKDENTGYIYEDTNNLNKDYQITTKRFTTGTDLKGYLLILKSONDEAMGD 660
QY 660 NFIISEIRPSEBELSPELIKSDAWVSGQTWISGNSLAINSVNGTPRONLSLSYSTYS 719
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 661 NFIISEIRPSEBELSPELIKSDAWVSGQTWISGNSLAINSVNGTPRONLSLSYSTYS 720
QY 720 MNFVNGPFGVYTIINSREVEERSYLOFSKYISEKFTTTNTGLYVELSRASS--RG 776
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 721 VYFVSQSDANVRINSREVELEKRYMS-GAKDVSEMFTEKONFYIELSQNNLVGGP 779
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 777 VINQDPSIK 786
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 780 IVHFYDVSIK 789
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RESULT 11

US-08-960-780-8
Sequence 8, Application US/08960780
Patent No. 6204435
GENERAL INFORMATION:
APPLICANT: Feltelson, Jerald S.
APPLICANT: Schnepf, H. Ernest

```

: APPLICANT: Narva, Kenneth E.
: APPLICANT: Stockhoff, Brian A.
: APPLICANT: Schoeifs, James
: APPLICANT: Loewer, David
: APPLICANT: Dullum, Charles Joseph
: APPLICANT: Muller-Cohn, Judy
: TITLE OF INVENTION: No. 6204435el Pesticidal Toxins and Nucleotide
: TITLE OF INVENTION: Sequences Which Encode These Toxins
: NUMBER OF SEQUENCES: 134
: CORRESPONDENCE ADDRESS:
: ADDRESS: Saliwanchik, Lloyd & Saliwanchik
: STREET: 2421 N.W. 41st Street, Suite A-1
: CITY: Gainesville
: STATE: FL
: COUNTRY: US
: ZIP: 32606-6669
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/960,780
: FILING DATE: 30-OCT-1997
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/029,848
: FILING DATE: 30-OCT-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Saliwanchik, David R.
: REGISTRATION NUMBER: 31,794
: REFERENCE/DOCKET NUMBER: MA-708
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 352-375-8100
: TELEFAX: 352-372-5800
: INFORMATION FOR SEQ ID NO: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 790 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: ORIGINAL SOURCE:
: INDIVIDUAL ISOLATE: Jav90
: US-08-960-780-8

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Query Match 79.5%; Score 3175.5; DB 2; Length 790;
Best Local Similarity 78.6%; Pred. No. 3.1e-216;
Matches 621; Conservative 70; Mismatches 94; Indels 5; Gaps 3;

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QY 1 MOKNN-KLSYKALPSFIDYNGIYGFATGIDIMNMIKFTNTGGDLTLDELTKNOQLNE 59
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Db 1 MNKNNTKLSARALPSFIDYNGIYGFATGIDIMNMIKFTNTGGDLTLDELTKNOQLNE 60
QY 60 ISGLDGVNGSLNDLDAQNLDTLSKEIILKIANEQKVNDVNTKDAINMLNTYLPK 119
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Db 61 ISGLDGVNGSLNDLDAQNLDTLSKEIILKIANEQKVNDVNTKDAINMLNTYLPK 120
QY 120 ITSMUSDVMKONVALSIQIEYLSKQLEISDKLDVINNVNLINSTLEITPAYORIKYVN 179
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QY 180 EKFEALTSATETNKTQDSSHTDIDDELTELTELAKSVTKNDVDGFEFYANTFHDVWG 239
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Db 181 EKFEALTSATETNKTQDSSHTDIDDELTELTELAKSVTKNDVDGFEFYANTFHDVWG 240
QY 240 NNLFGRSALKTASSELIAKENLKTSGSEVGVNPNFLIYLTALQAKAFLLTTCRKLGLAD 299
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 241 NNLFGRSALKTASSELIAKENLKTSGSEVGVNPNFLIYLTALQAKAFLLTTCRKLGLAD 300
QY 300 IDYTPINNEHLNKEKEEFVNILPTLSNTFSNPNYEKARSGDKAKIMEAKPGYALVGF 359
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

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Db 301 IDYTSIMNEHLNKEKEEFVNIPTLSNTFSPNPYAKVGSDEDAKMIVEAKPGHALIGF 360
Qy 360 EISKDSIAVLKYQAKLKHNYQIDKDSLEIYVGIDKLCPPDSEOMYTNKIAFPNEY 419
Db 361 EISNDSITVLKYEAQKQYQVQKDSLEIYVGMKLCPPDSEQIYTNNIYVFPNEY 420
Qy 420 VITKIAFTKLSIRYEVTANFYDSSTGDIIDLNKKKIESSEAFSMNANNQVYMEIGT 479
Db 421 VITKIDFTKQKMTIRYEVTANFYDSSTGEIDLNKKKVESSEAFRTLSANDGYMPLGV 480
Qy 480 ISEFTLPINGFGLVVDENSRLVTLTKSYARETLATDLSNKKTKIYPPNGISNIYE 539
Db 481 ISEFTLPINGFGLQADENSRLVTLTKSYARETLATDLSNKKTKIYPPSGFISNIYE 540
Qy 540 NGNLGEMLEPWKANNKAAVYDHTGVNGTKVLYVHDEGEFQFIDGDKLKTEYVIOYI 599
Db 541 NGSTIEDNLEPWKANNKAAVYDHTGVNGTKVLYVHODGGSQITGDKLKTEYVIOYT 600
Qy 600 VKGKAIIYLKDEKNGDIYEBETNNELEDFQAVTKRFTGTDSRVHLIFTSONGEBAFG 659
Db 601 VKGKPSIHLKDEMTGYIHYEDTNNLEDTYQINRFTGTGDLKGVYLIILKSQNGDEAMGD 660
Qy 660 NFIISEIRPSEELSPELIKSDAWVSGQTIWISGNSLINSNVNGTFRONLSLESYTYS 719
Db 661 NFIIIEISPSEKLSPELINTNMTSTGSTINISGNTILTYOGGRGILKONQJLDSFSTYR 720
Qy 720 MNFVNGFGKVTIRNSREVFERSYLOFSSKYISEKFTTNTNGLVVELSRASS---RG 776
Db 721 VYFSVSDANVRIRNSREVFERSYLOFSSKYISEKFTTNTNGLVVELSRASS---RG 779
Qy 777 VINFGDSIK 786
Db 780 IVHFYDVSIK 789

RESULT 12
US-09-073-898-8
Sequence 8, Application US/09073898
Patent No. 6242669
GENERAL INFORMATION:
APPLICANT: Feltelson, Gerald S.
APPLICANT: Schnef, H. Ernest
APPLICANT: Narva, Kenneth E.
APPLICANT: Stockhoff, Brian A.
APPLICANT: Schmeltz, James
APPLICANT: Loewer, David
APPLICANT: Dullum, Charles Joseph
APPLICANT: Muller-Cohn, Judy
APPLICANT: Stamp, Lisa
APPLICANT: Morrill, George
APPLICANT: Finstad-Lee, Stacey
TITLE OF INVENTION: No. 6242669el Pepticidal Toxins and Nucleotide
TITLE OF INVENTION: Sequences which Encode These Toxins
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: US
ZIP: 32606-6669
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,898
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,848
FILING DATE: 30-OCT-1996

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/960,780
FILING DATE: 30-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-708C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
TELEFAX: 352-372-5800
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 790 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Jav90
US-09-073-898-8

Query Match 79.5%; Score 3175.5; DB 2; length 790;
Best Local Similarity 78.6%; Pred. No. 3,1e-216;
Matches 62; Conservative 70; Mismatches 94; Indels 5; Gaps 3;

Qy 1 MOKM-KLSVKALPSFTIDYFNNGIYGFATGKIDIMNIKFTNTGSDTLDEILKNOOLNE 59
Db 1 MNKNNTKLSRALPSFTIDYFNNGIYGFATGKIDIMNIKFTNTGSDTLDEILKNOOLNE 60
Qy 60 ISGKLDGVNGSLNDLAAQGNLDELSEKELIKIANEQNKYLDVNTGLDAINMLANTYLPK 119
Db 61 ISGKLDGVNGSLNDLAAQGNLDELSEKELIKIANEQNKYLDVNTGLDAINMLANTYLPK 120
Qy 120 ITSMLSDVNKQNYALGLQIEYLSKQIKESDKLDVINAVNLINSTLTBITPAYORIKYVN 179
Db 121 ITSMLSDVNKQNYALGLQIEYLSKQIKESDKLDVINAVNLINSTLTBITPAYORIKYVN 180
Qy 180 EKFEALTSATENTMLTKKODSSHDLDELTELTELAKSTYKNDVDFEFTYNTFHVVMIG 239
Db 181 EKFEELTPAFETSSKVKKDGSPADLDDELTELTELAKSTYKNDVDFEFTYNTFHVVMIG 240
Qy 240 NMLFGSALKTASELAKENLKTSGSEGVNVAFLVLTALQAKAFLLTTTCRKLGLAD 299
Db 241 NMLFGSALKTASELAKENLKTSGSEGVNVAFLVLTALQAKAFLLTTTCRKLGLAD 300
Qy 300 IDYTPIMNEHLNKEKEEFVNIPTLSNTFSPNPYAKVGSDEDAKMIVEAKPGHALIGF 359
Db 301 IDYTSIMNEHLNKEKEEFVNIPTLSNTFSPNPYAKVGSDEDAKMIVEAKPGHALIGF 360
Qy 360 EISKDSIAVLKYQAKLKHNYQIDKDSLEIYVGIDKLCPPDSEOMYTNKIAFPNEY 419
Db 361 EISNDSITVLKYEAQKQYQVQKDSLEIYVGMKLCPPDSEQIYTNNIYVFPNEY 420
Qy 420 VITKIAFTKLSIRYEVTANFYDSSTGDIIDLNKKKIESSEAFSMNANNQVYMEIGT 479
Db 421 VITKIDFTKQKMTIRYEVTANFYDSSTGEIDLNKKKVESSEAFRTLSANDGYMPLGV 480
Qy 480 ISEFTLPINGFGLVVDENSRLVTLTKSYARETLATDLSNKKTKIYPPNGISNIYE 539
Db 481 ISEFTLPINGFGLQADENSRLVTLTKSYARETLATDLSNKKTKIYPPSGFISNIYE 540
Qy 540 NGNLGEMLEPWKANNKAAVYDHTGVNGTKVLYVHDEGEFQFIDGDKLKTEYVIOYI 599
Db 541 NGSTIEDNLEPWKANNKAAVYDHTGVNGTKVLYVHODGGSQITGDKLKTEYVIOYT 600
Qy 600 VKGKAIIYLKDEKNGDIYEBETNNELEDFQAVTKRFTGTDSRVHLIFTSONGEBAFG 659
Db 601 VKGKPSIHLKDEMTGYIHYEDTNNLEDTYQINRFTGTGDLKGVYLIILKSQNGDEAMGD 660
Qy 660 NFIISEIRPSEELSPELIKSDAWVSGQTIWISGNSLINSNVNGTFRONLSLESYTYS 719
Db 661 NFIIIEISPSEKLSPELINTNMTSTGSTINISGNTILTYOGGRGILKONQJLDSFSTYR 720

Qy 720 MNFVNGFGKVTIRNSREVERSYLOFSSKYSIEKFTTTNNGLVVELSRASS---RG 776
Db 721 VYFVSQDANVRIRNSREVLFEKRYMS-GAKDVSEMTTKEKONFYIELSQGNLVGCP 779

Qy 777 VINFGDPSIK 786
Db 780 IVHFYDVSIK 789

RESULT 13

US-09-307-106-2
Sequence 2, Application US/09307106
Patent No. 6603063
GENERAL INFORMATION:
APPLICANT: Felteleon, Jerald S.
APPLICANT: Schnepf, H. Ernest
APPLICANT: Narva, Kenneth E.
APPLICANT: Stockhoff, Brian A.
APPLICANT: Schmeits, James
APPLICANT: Loewer, David
APPLICANT: Dullum, Charles Joseph
APPLICANT: Muller-Cohn, Judy
APPLICANT: Stamp, Lisa
APPLICANT: Morrill, George
APPLICANT: Finstead-Lee, Stacey
TITLE OF INVENTION: No. 6603063el Pesticidal Toxins and Nucleotide
TITLE OF INVENTION: Sequences Which Encode These Toxins
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: US
ZIP: 32606-6669
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/307,106
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,848
FILING DATE: 30-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/960,780
FILING DATE: 30-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/073,898
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-708C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
TELEFAX: 352-372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 790 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: protein
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Jav90
US-09-307-106-2
Query Match 79.5%; Score 3175.5; DB 2; Length 790;
Best Local Similarity 78.6%; Pred. No. 3.1e-216;

Matches 621; Conservative 70; Mismatches 94; Indels 5; Gaps 3;

Qy 1 MOKNN-KLSYKALPSFIDYENGIGYGFATGKIDIMNMFKNTGGDLTLDELKNOQLNE 59
Db 1 MNKNYLSSTRALPSFIDYENGIGYGFATGKIDIMNMFKNTGGDLTLDELKNOQLNE 60
Qy 60 ISGKLDGNSLNDLQAQNLDTLSKEIKIANEQKRVANDVTKDAINLMNTYLPK 119
Db 61 ISGKLDGNSLNDLQAQNLDTLSKEIKIANEQKRVANDVTKDAINLMNTYLPK 120
Qy 120 ITSMVDMKONTALGLQIEYLSKOLKEISDKLDVINNVNLINSTLTTPAYORIRYVN 179
Db 121 ITSMVDMKONTALGLQIEYLSKOLKEISDKLDVINNVNLINSTLTTPAYORIRYVN 180
Qy 180 EKPEALTSATETNKTQDSSHNDILDELTELTELASVTKNDVGEFYNTHDMIG 239
Db 181 EKPEALTSATETNKTQDSSHNDILDELTELTELASVTKNDVGEFYNTHDMIG 240
Qy 240 NNLFGRSALKTASSELINKENIKTSGSEVGNVNFILVTLQAQAFLLTTCRKLGLAD 299
Db 241 NNLFGRSALKTASSELINKENIKTSGSEVGNVNFILVTLQAQAFLLTTCRKLGLAD 300
Qy 300 IDYTPINNEHLNKEKEEFVNVILPTLSNTESNPYERKAGSDKDAKIMEAKPGYALVGF 359
Db 301 IDYTSINNEHLNKEKEEFVNVILPTLSNTESNPYERKAGSDKDAKIMEAKPGYALVGF 360
Qy 360 EISKDSIALVAKYQAKIKHNYQDKSLSEIVGDDIKLCPDQSEDMYTTNKIAFNEY 419
Db 361 EISKDSITVAKYQAKIKHNYQDKSLSEIVGDDIKLCPDQSEDMYTTNKIAFNEY 420
Qy 420 VITKIAFTKQNSLRVEYTNFVDSSTGDIIDLNKKIKESSEAEPSMLNANDGVMPIGT 479
Db 421 VITKIDFTKQKTRIRYVTNANFVDSSTGDIIDLNKKIKESSEAEPSMLNANDGVMPIGT 480
Qy 480 ISETFTLPINGFGLVVDENSRLVTLTKSYLRETLATDLSNRETKLIVPNEGFSINIVE 539
Db 481 ISETFTLPINGFGLVVDENSRLVTLTKSYLRETLATDLSNRETKLIVPNEGFSINIVE 540
Qy 540 NGNLEGENLEPPKANNNAVVDHTGNGKRLVYHEDGFSQFQKGLKTEYVVOYI 599
Db 541 NGNLEGENLEPPKANNNAVVDHTGNGKRLVYHEDGFSQFQKGLKTEYVVOYI 600
Qy 600 VKGKAIFYLDEKNGDIYEETNNELEDFOATKRFITGDSRVHLIFTSNGEBAFGG 659
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Qy 660 NFIISEIRPEBELSPELIKSDAMVGSQGTWISGNSLINSNVNGTRONLSIESYSTYS 719
Db 661 NFIISEIRPEBELSPELIKSDAMVGSQGTWISGNSLINSNVNGTRONLSIESYSTYS 720
Qy 720 MNFVNGFGKVTIRNSREVERSYLOFSSKYSIEKFTTTNNGLVVELSRASS---RG 776
Db 721 VYFVSQDANVRIRNSREVLFEKRYMS-GAKDVSEMTTKEKONFYIELSQGNLVGCP 779
Qy 777 VINFGDPSIK 786
Db 780 IVHFYDVSIK 789

RESULT 14

US-09-650-351A-8
Sequence 8, Application US/09850351A
Patent No. 6656908
GENERAL INFORMATION:
APPLICANT: Felteleon, Jerald S.
APPLICANT: Schnepf, H. Ernest
APPLICANT: Narva, Kenneth E.
APPLICANT: Stockhoff, Brian A.
APPLICANT: Schmeits, James
APPLICANT: Loewer, David
APPLICANT: Dullum, Charles Joseph
APPLICANT: Muller-Cohn, Judy
APPLICANT: Stamp, Lisa

APPLICATION NUMBER: US 08/037,057
FILING DATE: 25-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: P-40,403
REFERENCE/DOCKET NUMBER: CGC 1695/CIP3/DIV7 - SOLV3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8582
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 789 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-471-033-29

Query Match 79.4%; Score 3171.5; DB 1; Length 789;

Best Local Similarity 78.5%; Pred. No. 6e-216;
Matches 620; Conservative 71; Mismatches 94; Indels 5; Gaps 3;

QY 1 MOKN-KLSVKALPSFIDYFNGIYGFATGIDIMNMIFKNTGGDLTLDLILKNQQLNE 59
DB 1 MNKNNTLSTRALPSFIDYFNGIYGFATGIDIMNMIFKNTGGDLTLDLILKNQQLNE 60
QY 60 ISGLDGVNGSLNDLDAQNDTELSEKILKIANEONKVLNDVNTKLDATNMTYLPK 119
DB 61 ISGLDGVNGSLNDLDAQNDTELSEKILKIANEONKVLNDVNTKLDATNMTYLPK 120
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DB 181 EKPEALTSATETNKTQDSHMDLDELTELTAASVTXNDVDGFEFYINTFHDVIG 240
QY 240 NNLFGRSALKTASSELKENLKTSGSEVGVNPNFLIVTLALQAKFLTLTCRLGLAD 299
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DB 301 IDYTPINNEHLNKEKEFRVNIILPTLSNTSPNPNYEXARSGSDKAKIMEAKPGYALVGF 360
QY 360 EISGDSIAVLKVTYQAKIKANYQIDKSLSEIYVGDIDKLCPDQSEQMYTNTKIAPNEY 419
DB 361 EISGDSIAVLKVTYQAKIKANYQIDKSLSEIYVGDIDKLCPDQSEQMYTNTKIAPNEY 420
QY 420 VITKIAFTKLNLSRYEVTANPVDSSGTGDDIDNKKKIESSEAEFSMTANNDGYMPIGT 479
DB 421 VITKIDFTKMKTLRYEVTANPVDSSGTGDDIDNKKKIESSEAEFSMTANNDGYMPIGT 480
QY 480 ISEFTLPINGFGIYVDENSRLVTLTCKSYLRETLATDLSNKETKLIIVPNGFISNIVE 539
DB 481 ISEFTLPINGFGIYVDENSRLVTLTCKSYLRETLATDLSNKETKLIIVPNGFISNIVE 540
QY 540 NGNLEGENLEPPKANNQNAVYDHTGVNGTKVLYVHEDGEPQFISGDKLAKTEYVIOYI 599
DB 541 NGNLEGENLEPPKANNQNAVYDHTGVNGTKVLYVHEDGEPQFISGDKLAKTEYVIOYI 600
QY 600 VKGKAAYLDEKNGDVIYEETNNLEDPQAVTKRFITGTDSSRVHLIFTSQNGEBAFGG 659
DB 601 VKGKAAYLDEKNGDVIYEETNNLEDPQAVTKRFITGTDSSRVHLIFTSQNGEBAFGG 660
QY 660 NFIISEIRPEBELSPELIKSDAVVGSQGTWISGNSLINSNVNGTFPRQNLSESYSTYS 719
DB 661 NFIISEIRPEBELSPELIKSDAVVGSQGTWISGNSLINSNVNGTFPRQNLSESYSTYS 720
QY 720 MNRVNGFGKVTITNSREVVPERSYLOPSSKIYSEKFTTTNTNTGLYVELSPASS--RG 776
DB 721 MNRVNGFGKVTITNSREVVPERSYLOPSSKIYSEKFTTTNTNTGLYVELSPASS--RG 777

QY 777 VINQDPSIK 786
DB 780 IVHFYDVSIX 789

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Job time : 50 sec

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GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 15, 2006, 20:44:16 ; Search time 168 Seconds
(without alignments)
1954.844 Million cell updates/sec

Title: US-10-698-096-17
Perfect score: 3995
Sequence: 1 MQGNKLSVYALPSFIDYFN.....VELSRASSRGVINGDFSIK 786

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.Main:*
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3995	100.0	786	4	US-10-698-096-17 Sequence 17, Appl
2	3507.5	87.8	787	4	US-10-473-687-2 Sequence 2, Appl
3	3507.5	87.8	787	5	US-10-505-315-7 Sequence 7, Appl
4	3505	87.7	787	4	US-10-452-002A-54 Sequence 54, Appl
5	3505	87.7	787	4	US-10-698-096-25 Sequence 25, Appl
6	3505	87.7	788	4	US-10-698-096-27 Sequence 27, Appl
7	3499.5	87.6	787	4	US-10-473-687-7 Sequence 7, Appl
8	3243.5	81.2	788	5	US-10-505-315-32 Sequence 32, Appl
9	3239	81.1	788	5	US-10-505-315-2 Sequence 2, Appl
10	3235	81.0	788	5	US-10-505-315-11 Sequence 11, Appl
11	3182.5	79.7	789	4	US-10-099-285-82 Sequence 82, Appl
12	3180.5	79.6	789	4	US-10-099-285-84 Sequence 84, Appl
13	3176.5	79.5	789	4	US-10-099-285-92 Sequence 92, Appl
14	3175.5	79.5	789	4	US-10-473-687-5 Sequence 5, Appl
15	3175.5	79.5	789	5	US-10-505-315-5 Sequence 5, Appl
16	3175.5	79.5	790	3	US-09-850-351A-8 Sequence 8, Appl
17	3175.5	79.5	790	4	US-10-452-002A-2 Sequence 2, Appl
18	3175.5	79.5	790	4	US-10-698-096-8 Sequence 8, Appl
19	3172.5	79.4	786	4	US-10-698-096-19 Sequence 19, Appl
20	3171.5	79.4	789	3	US-09-904-226-2 Sequence 2, Appl
21	3170.5	79.4	789	4	US-10-099-285-78 Sequence 78, Appl
22	3170.5	79.4	789	4	US-10-099-285-94 Sequence 94, Appl
23	3170.5	79.4	789	4	US-10-099-285-96 Sequence 96, Appl
24	3167.5	79.3	789	3	US-09-850-351A-6 Sequence 6, Appl
25	3167.5	79.3	789	4	US-10-698-096-6 Sequence 6, Appl
26	3158.5	79.1	790	3	US-09-850-351A-4 Sequence 4, Appl
27	3158.5	79.1	790	4	US-10-698-096-4 Sequence 4, Appl

28	3156.5	79.0	789	3	US-09-904-226-4 Sequence 4, Appl
29	3151	78.9	790	4	US-10-099-285-102 Sequence 102, App
30	3149.5	78.8	789	4	US-10-099-285-98 Sequence 98, Appl
31	3132.5	78.4	789	4	US-10-099-285-90 Sequence 90, Appl
32	3130.5	78.4	789	4	US-10-099-285-100 Sequence 100, App
33	3083.5	77.2	789	4	US-10-099-285-80 Sequence 80, Appl
34	3073.5	76.9	746	3	US-09-904-226-6 Sequence 6, Appl
35	2423.5	60.7	759	4	US-10-099-285-86 Sequence 86, Appl
36	2405.5	60.2	801	5	US-10-505-315-9 Sequence 9, Appl
37	2233	55.9	511	4	US-10-099-285-88 Sequence 88, Appl
38	208.5	5.2	2539	5	US-10-831-070-6 Sequence 6, Appl
39	205.5	5.1	2265	4	US-10-282-122A-45123 Sequence 45123, A
40	203.5	5.1	1315	5	US-10-744-672-5 Sequence 5, Appl
41	203.5	5.1	1315	5	US-10-744-616-5 Sequence 5, Appl
42	203.5	5.1	1315	5	US-10-470-048B-124 Sequence 124, App
43	195.5	4.9	3533	4	US-10-282-122A-70177 Sequence 70177, A
44	194.5	4.9	1349	3	US-09-815-242-5898 Sequence 5898, Ap
45	194.5	4.9	1349	3	US-09-815-242-13137 Sequence 13137, A

ALIGNMENTS

```
RESULT 1
US-10-698-096-17
; Sequence 17, Application US/10698096
; Publication No. US20040128716A1
; GENERAL INFORMATION:
; APPLICANT: Narva, Kenneth
; TITLE OF INVENTION: Polynucleotides, Pesticidal Proteins, and Novel Methods of Using
; FILE REFERENCE: MA-708C0C1
; CURRENT APPLICATION NUMBER: US/10/698,096
; PRIOR FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: US 09/850,351
; PRIOR FILING DATE: 2001-05-07
; PRIOR APPLICATION NUMBER: US 09/073,898
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: US 08/690,780
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 60/029,848
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 786
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-698-096-17

Query Match      100.0%; Score 3995; DB 4; Length 786;
Best Local Similarity 100.0%; Pred. No. 1.1e-236;
Matches 786; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MQGNKLSVYALPSFIDYFNIGYGFATGKDIWNMI FKNITGSDLTLDRLKNOQLNRI 60
      |||||||
DB      1  MQGNKLSVYALPSFIDYFNIGYGFATGKDIWNMI FKNITGSDLTLDRLKNOQLNRI 60

QY      61  SGRLDVGNSLNDLDAQNLDTLSTKEILKIANEQNKVINDVTKDAINLMNTYLPKI 120
      |||||||
DB      61  SGRLDVGNSLNDLDAQNLDTLSTKEILKIANEQNKVINDVTKDAINLMNTYLPKI 120

QY      121 TSWLSVDMKQNYALGQIEYLSQQLKEISDKLDVINNVNLINSTLTETIPAYORIKYVN 180
      |||||||
DB      121 TSWLSVDMKQNYALGQIEYLSQQLKEISDKLDVINNVNLINSTLTETIPAYORIKYVN 180

QY      181 KPEALTSATETNKTQKDSHTDILDELTELTELASVTKNDVGEFPLNTFHDWIGN 240
      |||||||
DB      181 KPEALTSATETNKTQKDSHTDILDELTELTELASVTKNDVGEFPLNTFHDWIGN 240

QY      241 NLFGRSALTYASLTKENLTKTSGSEVGNVNFLLVTLTLOAKAFLLTTCRGLGIADI 300
      |||||||
DB      241 NLFGRSALTYASLTKENLTKTSGSEVGNVNFLLVTLTLOAKAFLLTTCRGLGIADI 300
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QY 301 DYPIMNEHINKKEEFVNILPTLSNTPSNPYEKAGSDKAKIIMEAKPGYALVGF 360
DB 301 DYPIMNEHINKKEEFVNILPTLSNTPSNPYEKAGSDKAKIIMEAKPGYALVGF 360
QY 361 ISKDSIAVLKYYOAKLKHNQIDKDSISEIYVGDIDKLLCPDQSEQMYTNKLAFPNEY 420
DB 361 ISKDSIAVLKYYOAKLKHNQIDKDSISEIYVGDIDKLLCPDQSEQMYTNKLAFPNEY 420
QY 421 ITTIAFPKKNLSRYEVTANFYDSSGTDIDLNKKKISSSEAFSMLNANDGYMPTGTT 480
DB 421 ITTIAFPKKNLSRYEVTANFYDSSGTDIDLNKKKISSSEAFSMLNANDGYMPTGTT 480
QY 481 SETFLPPIINGFGLVVDENSLVTLTCKSYLRETLATDLSNKETKLIIVPNGFISNIYEN 540
DB 481 SETFLPPIINGFGLVVDENSLVTLTCKSYLRETLATDLSNKETKLIIVPNGFISNIYEN 540
QY 541 GNLEGENLEPMKANNKNAAYVDHTGYNVTGYLVEHDEFSQFIDGDKLKTEYVYQYIY 600
DB 541 GNLEGENLEPMKANNKNAAYVDHTGYNVTGYLVEHDEFSQFIDGDKLKTEYVYQYIY 600
QY 601 KGRKAIYLDKRNKGDYIYEETNNLEDFQAVTRKFTTGDS SRVHLIFTSQNGEAPFGN 660
DB 601 KGRKAIYLDKRNKGDYIYEETNNLEDFQAVTRKFTTGDS SRVHLIFTSQNGEAPFGN 660
QY 661 FIISIRPSEBELSPELIKSDAWGSGQTIWISGNSLNINSVNGTFRONLSLESYSTYS 720
DB 661 FIISIRPSEBELSPELIKSDAWGSGQTIWISGNSLNINSVNGTFRONLSLESYSTYS 720
QY 721 NFNVNGFGKVTIRNSREVEVFRSYLOFSSKYISEKFTTTNNNGLYVELSRASSRGVIN 780
DB 721 NFNVNGFGKVTIRNSREVEVFRSYLOFSSKYISEKFTTTNNNGLYVELSRASSRGVIN 780
QY 781 GDFSIX 786
DB 781 GDFSIX 786

RESULT 2

US-10-473-687-2
Sequence 2, Application US/10473687
Publication No. US2004013942A1
GENERAL INFORMATION:
APPLICANT: Miles, Paul
APPLICANT: Kramer, Vance
APPLICANT: Shen, Zhicheng
APPLICANT: Shokkoski, Frank
APPLICANT: Warren, Greg
TITLE OF INVENTION: Novel Pesticidal Toxins
FILE REFERENCE: S-60000PCT
CURRENT APPLICATION NUMBER: US/10/473,687
CURRENT FILING DATE: 2003-09-27
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 787
TYPE: PRT
ORGANISM: Bacillus thuringiensis
US-10-473-687-2

Query Match 87.8%; Score 3507.5; DB 4; Length 787;
Best Local Similarity 87.3%; Pred. No. 9, 8e-207;
Matches 687; Conservative 46; Mismatches 53; Indels 1; Gaps 1;
QY 1 MOKNN-KLSVKALPSFIDYFNGIYGFATGIKDIMNIFFNTTGGDLTDEILKNOQLNE 59
DB 1 MOKNN-KLSVKALPSFIDYFNGIYGFATGIKDIMNIFFNTTGGDLTDEILKNOQLNE 59
QY 60 ISGKLDGVNGSLNDLAAQGNLDTHELSEKELIKIANEQNKLVNVTGLDIAINMLNTYLPK 119
DB 60 ISGKLDGVNGSLNDLAAQGNLDTHELSEKELIKIANEQNKLVNVTGLDIAINMLNTYLPK 119
QY 61 ISGKLDGVNGSLNDLAAQGNLDTHELSEKELIKIANEQNKLVNVTGLDIAINMLNTYLPK 120
DB 61 ISGKLDGVNGSLNDLAAQGNLDTHELSEKELIKIANEQNKLVNVTGLDIAINMLNTYLPK 120
QY 120 ITSMUSDVWKQNVYALGLQIEYLSKQKEISDKLDVINVNVILNSTLTETTPAVQRIKYN 179

DB 121 ITSMUSDVWKQNVYALGLQIEYLSKQKEISDKLDVINVNVILNSTLTETTPAVQRIKYN 180
QY 180 EKFEALTSATEYNLTKYKODSSHDDIDBELTELAKSYTKODVDGFEFYLTAFHDVWG 239
DB 181 EKFEALTSATEYNLTKYKODSSHDDIDBELTELAKSYTKODVDGFEFYLTAFHDVWG 240
QY 240 NNLFGRSALKTASSELJAKENLTKSGSEGVNVPFLIVTALQAKAFLLTTCRKLLGLAD 299
DB 241 NNLFGRSALKTASSELJAKENLTKSGSEGVNVPFLIVTALQAKAFLLTTCRKLLGLAD 300
QY 300 IYTPIMNEHINKKEEFVNILPTLSNTPSNPYEKAGSDKAKIIMEAKPGYALVGF 359
DB 301 IYTPIMNEHINKKEEFVNILPTLSNTPSNPYEKAGSDKAKIIMEAKPGYALVGF 360
QY 360 EISKDSIAVLKYYOAKLKHNQIDKDSISEIYVGDIDKLLCPDQSEQMYTNKLAFPNEY 419
DB 361 EISKDSIAVLKYYOAKLKHNQIDKDSISEIYVGDIDKLLCPDQSEQMYTNKLAFPNEY 420
QY 420 VITTKIAFTKKNLSRYEVTANFYDSSGTDIDLNKKKISSSEAFSMLNANDGYMPTGTT 479
DB 421 VITTKIAFTKKNLSRYEVTANFYDSSGTDIDLNKKKISSSEAFSMLNANDGYMPTGTT 480
QY 480 ISETFLPPIINGFGLVVDENSLVTLTCKSYLRETLATDLSNKETKLIIVPNGFISNIYEN 539
DB 481 ISETFLPPIINGFGLVVDENSLVTLTCKSYLRETLATDLSNKETKLIIVPNGFISNIYEN 540
QY 540 NGNLEGENLEPMKANNKNAAYVDHTGYNVTGYLVEHDEFSQFIDGDKLKTEYVYQYI 599
DB 541 NGNLEGENLEPMKANNKNAAYVDHTGYNVTGYLVEHDEFSQFIDGDKLKTEYVYQYI 600
QY 600 VNGKAIYLDKRNKGDYIYEETNNLEDFQAVTRKFTTGDS SRVHLIFTSQNGEAPFGN 659
DB 601 VNGKAIYLDKRNKGDYIYEETNNLEDFQAVTRKFTTGDS SRVHLIFTSQNGEAPFGN 660
QY 660 NFISIRPSEBELSPELIKSDAWGSGQTIWISGNSLNINSVNGTFRONLSLESYSTYS 719
DB 661 NFISIRPSEBELSPELIKSDAWGSGQTIWISGNSLNINSVNGTFRONLSLESYSTYS 720
QY 720 NFNVNGFGKVTIRNSREVEVFRSYLOFSSKYISEKFTTTNNNGLYVELSRASSRGVIN 779
DB 721 NFNVNGFGKVTIRNSREVEVFRSYLOFSSKYISEKFTTTNNNGLYVELSRASSRGVIN 780
QY 780 FDFSIX 786
DB 781 FDFSIX 787

RESULT 3

US-10-505-315-7
Sequence 7, Application US/10505315
Publication No. US20050210545A1
GENERAL INFORMATION:
APPLICANT: Syngenta Participations AG
APPLICANT: Warren, Greg
APPLICANT: Shokkoski, Frank
APPLICANT: Kramer, Vance
TITLE OF INVENTION: Novel Vip3 Toxins and Methods of Use
FILE REFERENCE: 60163PCT
CURRENT APPLICATION NUMBER: US/10/505,315
CURRENT FILING DATE: 2004-08-19
PRIOR APPLICATION NUMBER: US 60/362250
SOFTWARE: Patentin version 3.2
SEQ ID NO 7
LENGTH: 787
TYPE: PRT
ORGANISM: Bacillus thuringiensis
NAME/KEY: MISC FEATURE
LOCATION: (1)..(787)

OTHER INFORMATION: vip3b Toxin
US-10-505-315-7

Query Match 87.8%; Score 3507.5; DB 5; Length 787;
Best Local Similarity 87.3%; Pred. No. 9.8e-207;
Matches 687; Conservative 46; Mismatches 53; Indels 1; Gaps 1;

QY 1 MORNN-KLSVYKALPSFIDYNGIYGFATGDKIDNMNMFKTNTGDLTLDELTKNQOULNE 59
DB 1 MNKNKLNARALPSFIDYNGIYGFATGDKIDNMNMFKTNTGDLTLDELTKNQOULNE 60
QY 60 ISGKLDGVNGSLNDLAQGNLDELTELSEIKIANEQNKVLDVNTKDAINMLNTYLPK 119
DB 61 ISGKLDGVNGSLNDLAQGNLDELTELSEIKIANEQNKVLDVNTKDAINMLNTYLPK 120
QY 120 ITSMLESDVMKONALGQIETLSKQLEISDKLDVINVNVLINSTLEIPAYORIKYVN 179
DB 121 ITSMLESDVMKONALGQIETLSKQLEISDKLDVINVNVLINSTLEIPAYORIKYVN 180
QY 180 EKEPALTSATETNLTAKTQDSHTDIDELTELTELAKSVTKNDVDFEFLANTFHDVMIG 239
DB 181 EKEPALTSATETNLTAKTQDSHTDIDELTELTELAKSVTKNDVDFEFLANTFHDVMIG 240
QY 240 NNIFGRSALKTASSELIAKENLKTSGSEVGNNVNFLLVLAQAKAFLLTTCRKLGLAD 299
DB 241 NNIFGRSALKTASSELIAKENLKTSGSEVGNNVNFLLVLAQAKAFLLTTCRKLGLAD 300
QY 300 IDYTPIMNHLNKEKEFRVNIILPTLSNTPSNPYEAKRSDDAKIMAKXGYALVGF 359
DB 301 IDYTPIMNHLNKEKEFRVNIILPTLSNTPSNPYEAKRSDDAKIMAKXGYALVGF 360
QY 360 EISKSDIAVLKVVQAKLKNNYQIDKQSLSEIYVGDIDKLCPOSSEOMYTNKLAIPNEX 419
DB 361 EISKSDIAVLKVVQAKLKNNYQIDKQSLSEIYVGDIDKLCPOSSEOMYTNKLAIPNEX 420
QY 420 VITTKLAFTKCLNSLRVEVTANFYDSSGTGIDIDNKKKIESSEAFSMNANDGVNPIGT 479
DB 421 VITTKLAFTKCLNSLRVEVTANFYDSSGTGIDIDNKKKIESSEAFSMNANDGVNPIGT 480
QY 480 ISFTFLTPINGFGLVVDENSLVTLTCKSYLRETLATDLSNKETKLIYPNPFISNIYE 539
DB 481 ISFTFLTPINGFGLVVDENSLVTLTCKSYLRETLATDLSNKETKLIYPNPFISNIYE 540
QY 540 NGNLEGENLEPMWANNKNAVYDHTGNGVNGTKVLYVHEDGEFSOFIGDKLKTETEYIYQYI 599
DB 541 NGNLEGENLEPMWANNKNAVYDHTGNGVNGTKVLYVHEDGEFSOFIGDKLKTETEYIYQYI 600
QY 600 VNGKALILYKDEKNGDIYIEETNNLEDFQAVTKRPIGTDSRVHLIFTSQNGEBAFGG 659
DB 601 VNGKALILYKDEKNGDIYIEETNNLEDFQAVTKRPIGTDSRVHLIFTSQNGEBAFGG 660
QY 660 NPLISIRSEBELLSPELLKSDAMVGSQGTWISGNSLNTSNVNGTRQNLSEISYTSY 719
DB 661 NPLISIRSEBELLSPELLKSDAMVGSQGTWISGNSLNTSNVNGTRQNLSEISYTSY 720
QY 720 MNPNVNGFGVGTIRNSREVVEFSYLOFSKYISEKRTTNTNGIYVELSRASSGVIN 779
DB 721 MNPNVNGFGVGTIRNSREVVEFSYLOFSKYISEKRTTNTNGIYVELSRASSGVIN 780
QY 780 FGDPSIK 786
DB 781 FGDPSIK 787

RESULT 4

US-10-452-002A-54
; Sequence 54, Application US/10452002A
; Publication No. US20030236195A1
; GENERAL INFORMATION:
; APPLICANT: Jerald S. Feltselson
; APPLICANT: H. Ernest Schmeft
; APPLICANT: Kenneth E. Narva
; APPLICANT: Brian A. Stockhoff

APPLICANT: James L. Schmeits
APPLICANT: David Joewer
APPLICANT: Charles J. Dullum
APPLICANT: Judy Muller-Cohn
APPLICANT: Lisa Stamp
APPLICANT: George Morill
APPLICANT: Stacey Finstad Lee
TITLE OF INVENTION: No. US20030236195A1el Pesticidal Proteins and Methods of Using 1
FILE REFERENCE: MA708C201
CURRENT APPLICATION NUMBER: US/10/452, 002A
CURRENT FILING DATE: 2003-05-30
PRIOR APPLICATION NUMBER: 09/307,106
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: 09/073, 898
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 08/960, 780
PRIOR FILING DATE: 1997-10-30
PRIOR APPLICATION NUMBER: 60/029, 848
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 54
LENGTH: 787
TYPE: PRT
ORGANISM: Bacillus thuringiensis strain KB59A4-6
US-10-452-002A-54

Query Match 87.7%; Score 3505; DB 4; Length 787;
Best Local Similarity 87.1%; Pred. No. 1.4e-206;
Matches 682; Conservative 45; Mismatches 56; Indels 0; Gaps 0;

QY 4 NNLKSVYKALPSFIDYNGIYGFATGDKIDNMNMFKTNTGDLTLDELTKNQOULNEISGK 63
DB 5 NNLKSVYKALPSFIDYNGIYGFATGDKIDNMNMFKTNTGDLTLDELTKNQOULNEISGK 64
QY 64 LDGVNGSLNDLAQGNLDELTELSEIKIANEQNKVLDVNTKDAINMLNTYLPKITSM 123
DB 65 LDGVNGSLNDLAQGNLDELTELSEIKIANEQNKVLDVNTKDAINMLNTYLPKITSM 124
QY 124 LSDVMKONALGQIETLSKQLEISDKLDVINVNVLINSTLEIPAYORIKYVNEKEFE 183
DB 125 LSDVMKONALGQIETLSKQLEISDKLDVINVNVLINSTLEIPAYORIKYVNEKEFE 184
QY 184 ALTSATETNLTAKTQDSHTDIDELTELTELAKSVTKNDVDFEFLANTFHDVMIGNLF 243
DB 185 ALTSATETNLTAKTQDSHTDIDELTELTELAKSVTKNDVDFEFLANTFHDVMIGNLF 244
QY 244 GRSALKTASSELIAKENLKTSGSEVGNNVNFLLVLAQAKAFLLTTCRKLGLADIDYT 303
DB 245 GRSALKTASSELIAKENLKTSGSEVGNNVNFLLVLAQAKAFLLTTCRKLGLADIDYT 304
QY 304 PIMNHLNKEKEFRVNIILPTLSNTPSNPYEAKRSDDAKIMAKXGYALVGFISK 363
DB 305 PIMNHLNKEKEFRVNIILPTLSNTPSNPYEAKRSDDAKIMAKXGYALVGFISK 364
QY 364 DSIAVLKVVQAKLKNNYQIDKQSLSEIYVGDIDKLCPOSSEOMYTNKLAIPNEXYITK 423
DB 365 DSIAVLKVVQAKLKNNYQIDKQSLSEIYVGDIDKLCPOSSEOMYTNKLAIPNEXYITK 424
QY 424 IAFTKCLNSLRVEVTANFYDSSGTGIDIDNKKKIESSEAFSMNANDGVNPIGTISFT 483
DB 425 IAFTKCLNSLRVEVTANFYDSSGTGIDIDNKKKIESSEAFSMNANDGVNPIGTISFT 484
QY 484 FLTPINGFGLVVDENSLVTLTCKSYLRETLATDLSNKETKLIYPNPFISNIYVNGNL 543
DB 485 FLTPINGFGLVVDENSLVTLTCKSYLRETLATDLSNKETKLIYPNPFISNIYVNGNL 544
QY 544 EGENLEPMWANNKNAVYDHTGNGVNGTKVLYVHEDGEFSOFIGDKLKTETEYIYQYIVK 603
DB 545 EGENLEPMWANNKNAVYDHTGNGVNGTKVLYVHEDGEFSOFIGDKLKTETEYIYQYIVK 604
QY 604 AAIYKDEKNGDIYIEETNNLEDFQAVTKRPIGTDSRVHLIFTSQNGEBAFGFNFI 663
DB 605 AAIYKDEKNGDIYIEETNNLEDFQAVTKRPIGTDSRVHLIFTSQNGEBAFGFNFI 664

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Db 605 ASIIYKDKKNENSIYEIINNDEGFQVTKRPIITGDSGCIHLIFTSQNGEAFGNGFI 664
Qy 664 SEIRSEELLSPDLIKSDAMVGSQGTWISGNSLINSVNGTFRONLSIESTYSMNFN 723
Db 665 SEIRSEELLSPDLIKSDAMVGSQGTWISGNSLINSVNGTFRONLPLESIYSTYMNFT 724
Qy 724 VNGFGKVTIRNSREVPERSYIQSSKTISEKFTTTNNGTGLYVELSRASRGVINFDP 783
Db 725 VNGFGKVTIRNSREVPERSYIQSSKTISEKFTTTNNGTGLYVELSRASRGVINFDP 784
Qy 784 SIK 786
Db 785 SIK 787

RESULT 5
US-10-698-096-25
; Sequence 25, Application US/10698096
; Publication No. US20040128716A1
; GENERAL INFORMATION:
; APPLICANT: Merio, Donald
; TITLE OF INVENTION: Polynucleotides, Pesticidal Proteins, and Novel Methods of Using
; FILE REFERENCE: MA-708CDCl
; CURRENT FILING DATE: 2003-10-31
; PRIOR FILING DATE: 2001-05-07
; PRIOR FILING DATE: 2001-05-07
; PRIOR FILING DATE: 2001-05-07
; PRIOR FILING DATE: 1998-05-06
; PRIOR FILING DATE: 1997-10-30
; PRIOR FILING DATE: 1996-10-30
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 787
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-698-096-25

Query Match 87.7%; Score 3505; DB 4; Length 787;
Best Local Similarity 87.1%; Pred. No. 1.4e-206;
Matches 682; Conservative 45; Mismatches 56; Indels 0; Gaps 0;

Qy 4 NKKLSVKALPSFIDYFNGIYGFATGIDIMNMIKFTNGDGLTIDELIKNOQLNEISGK 63
Db 5 NTKANARALPSFIDYFNGIYGFATGIDIMNMIKFTNGDGLTIDELIKNOQLNEISGK 64
Qy 64 LDGVNGSINDLLAOGNLDTELSKEILKIANEQNVLDVNTKLDALINMLNTYLPKITSM 123
Db 65 LDGVNGSINDLLAOGNLDTELSKEILKIANEQNVLDVNTKLDALINMLNTYLPKITSM 124
Qy 124 LSDVKQNYVALGLOEYLSKOLKEISDKLDVINNVNLINSTLTETTPAYQRIKYNEKEE 183
Db 125 LSDVKQNYVALSLQVEYLSKOLKEISDKLDVINNVNLINSTLTETTPAYQRIKYNEKEE 184
Qy 184 ALTGATETNNLKTQDSSHTDILDELTELTAKSTKNDVDFEYIANTFHDMAGNULF 243
Db 185 ELTFATETTLTKVKQDSSPADILDELTELTAKSTKNDVDFEYIANTFHDMAGNULF 244
Qy 244 GRSALKTASELIAKENLKTSGSEVGNVNFILVLTALQAKAFILITTRKQLGLADIDYT 303
Db 245 GRSALKTASELIAKENVKTSGSEVGNVNFILVLTALQAKAFILITTRKQLGLADIDYT 304
Qy 304 PYNNEHLNKEKEEPPRVNLTPLSNTFSNPNTYKAGSDKAKIIMEAKGYALVGFELISK 363
Db 305 SINMEHLNKEKEEPPRVNLTPLSNTFSNPNTYKAGSDKAKIIMEAKGYALVGFELISK 364
Qy 364 DSIAVLTKYQAKLKNYQIDKDSLEIYQDIDKLLCPDQSEQMYNTKIAFPNEYVITK 423
Db 365 DSMITVLKYVEAKLKNYQVDDKDSLEIYQDIDKLLCPDQSEQMYNTKIAFPNEYVITK 424
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Qy 424 IATFKLNSIAREYEVANFYDSTGIDLNKKKIESSEAFSMNLANNNDGVMPIGTSET 483
Db 425 IDFTKMKTLAREYEVANSYDSTGIDLNKKKIESSEAFSMNLANNNDGVMPIGTSET 484
Qy 484 FLTPINGFGLVVDENSRVLTLTCKSYLRETLTATDLSNKEKYLIVPENGFSINVENGL 543
Db 485 FLTPINGFGLVVDENSRVLTLTCKSYLRETLTATDLSNKEKYLIVPISFINVENGL 544
Qy 544 EGENLEPMWANKKNAVYVHTGTGNGTKYLYHEDDEFQFIDKLTAKTEYIYQYVKKK 603
Db 545 EGENLEPMWANKKNAVYVHTGTGNGTKYLYHEDDEFQFIDKLTAKTEYIYQYVKKK 604
Qy 604 AAIYKDEKNGDIYIETNNLEDFQAVTKRPIITGDSRGVHLIFTSQNGEAFGNGFI 663
Db 605 ASIIYKDKKNENSIYEIINNDEGFQVTKRPIITGDSGCIHLIFTSQNGEAFGNGFI 664
Qy 664 SEIRSEELLSPDLIKSDAMVGSQGTWISGNSLINSVNGTFRONLSIESTYSMNFN 723
Db 665 SEIRSEELLSPDLIKSDAMVGSQGTWISGNSLINSVNGTFRONLPLESIYSTYMNFT 724
Qy 724 VNGFGKVTIRNSREVPERSYIQSSKTISEKFTTTNNGTGLYVELSRASRGVINFDP 783
Db 725 VNGFGKVTIRNSREVPERSYIQSSKTISEKFTTTNNGTGLYVELSRASRGVINFDP 784
Qy 784 SIK 786
Db 785 SIK 787
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RESULT 6
US-10-698-096-27
; Sequence 27, Application US/10698096
; Publication No. US20040128716A1
; GENERAL INFORMATION:
; APPLICANT: Merio, Donald
; TITLE OF INVENTION: Polynucleotides, Pesticidal Proteins, and Novel Methods of Using
; FILE REFERENCE: MA-708CDCl
; CURRENT FILING DATE: 2003-10-31
; PRIOR FILING DATE: 2001-05-07
; PRIOR FILING DATE: 2001-05-07
; PRIOR FILING DATE: 2001-05-07
; PRIOR FILING DATE: 1998-05-06
; PRIOR FILING DATE: 1997-10-30
; PRIOR FILING DATE: 1996-10-30
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 788
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-698-096-27
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Query Match 87.7%; Score 3505; DB 4; Length 788;
Best Local Similarity 87.1%; Pred. No. 1.4e-206;
Matches 682; Conservative 45; Mismatches 56; Indels 0; Gaps 0;

Qy 4 NKKLSVKALPSFIDYFNGIYGFATGIDIMNMIKFTNGDGLTIDELIKNOQLNEISGK 63
Db 6 NTKANARALPSFIDYFNGIYGFATGIDIMNMIKFTNGDGLTIDELIKNOQLNEISGK 65
Qy 64 LDGVNGSINDLLAOGNLDTELSKEILKIANEQNVLDVNTKLDALINMLNTYLPKITSM 123
Db 66 LDGVNGSINDLLAOGNLDTELSKEILKIANEQNVLDVNTKLDALINMLNTYLPKITSM 125
Qy 124 LSDVKQNYVALGLOEYLSKOLKEISDKLDVINNVNLINSTLTETTPAYQRIKYNEKEE 183
Db 126 LSDVKQNYVALSLQVEYLSKOLKEISDKLDVINNVNLINSTLTETTPAYQRIKYNEKEE 185
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QY 184 ALTSATETNKTQDSSHTDILDELTELTLASVTKNVDGFEFYLTNTHDVMIGNL 243
DB 186 ELFPATETTLKVKQDSSPADILDELTELTLASVTKNVDGFEFYLTNTHDVMIGNL 245
QY 244 GRALKTASFLIAKENIKTSGSEVGNVNYFLVLTALQAKAFLLTTCRKLGLADIDYT 303
DB 246 GRALKTASFLIAKENIKTSGSEVGNVNYFLVLTALQAKAFLLTTCRKLGLADIDYT 305
QY 304 PINHEHLNKEKEEFVNIPLTSLNTPSNPNYKARGSDKDAKIMEAKPGVALVGEFISK 363
DB 306 SINHEHLNKEKEEFVNIPLTSLNTPSNPNYKARGSDKDAKIMEAKPGVALVGEFISN 365
QY 364 DSIAVLKQYQAKLKNYQIDKDSLSEIYVGDIDKLCPOSSEQMYTNKIAFPNEYITK 423
DB 366 DSMTVLKVEAKLKQYQVQDKSLSEVIYSDMDKLCPOSSEQMYTNKIAFPNEYITK 425
QY 424 IATTKLNSLRVETANFYDSSSTGDDIDLNKKKIESSEAEFSMANNNDGYMPTIGTSET 483
DB 426 IDFTKCKMKTLYRYVLANYSYDSSTGEIDLNKKKVESSEAEYRTLSANNNDGYMPLGVISFT 485
QY 484 FLTPINGFLVDENSRVLTLCCKSYLRETLATDLSNKEKTLVPPNGFISNIVENG 543
DB 486 FLTPINGFLQADENSRVLTLCCKSYLRETLATDLSNKEKTLVPPISISNIVENG 545
QY 544 EGENLEPMWANNKNAVYDHTGVNGTKVLYHEDGFSQFIDGKDKLKTBYVLYQYIKG 603
DB 546 EGENLEPMWANNKNAVYDHTGVNGTKVLYHEDGFSQFVGGKLSKTEYVLYQYIKG 605
QY 604 AATYLDKRNQDYIYETNNELDFQAVTKRFTTGDSRVHLIFTSQNGEBAFGNFII 663
DB 606 AATYLDKRNQDYIYETNNELDFQAVTKRFTTGDSRVHLIFTSQNGEBAFGNFII 665
QY 664 SEIRPEELLSPELIKSDAMVGSQGTWISGNSLNINSNVNGTFRONLSLESYSTYSNEN 723
DB 666 SEIRPEELLSPELIKSDAMVGSQGTWISGNSLNINSNVNGTFRONLSLESYSTYSNFT 725
QY 724 VNGFGKVTIRNSREVPERSYLOFSSKXISEKFTTTNNGLYVELSRASSRGVINFGDF 783
DB 726 VNGFGKVTIRNSREVPERSYLOFSSKXISEKFTTTNNGLYVELSRASSRGVINFRDF 785
QY 784 STK 786
DB 786 STK 788

RESULT 7
US-10-473-687-7
; Sequence 7, Application US/10473687
; Publication No. US20040133942A1
; GENERAL INFORMATION:
; APPLICANT: Miller, Paul
; APPLICANT: Kramer, Vance
; APPLICANT: Shen, Zhicheng
; APPLICANT: Shokkoski, Frank
; APPLICANT: Warren, Greg
; TITLE OF INVENTION: Novel Pesticidal Toxins
; FILE REFERENCE: S-60000PCT
; CURRENT APPLICATION NUMBER: US/10/473,687
; CURRENT FILING DATE: 2003-09-27
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 787
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(787)
; OTHER INFORMATION: Hybrid Vip3A-B Toxin
US-10-473-687-7

Query Match 87.6%; Score 3499.5; DB 4; Length 787;
Best Local Similarity 86.4%; Pred. No. 3e-206;
```

```
Matches 680; Conservative 49; Mismatches 57; Indels 1; Gaps 1;
QY 1 MCKN -CLSKALPSFIDYNGIYGATGATKDTMMI FKNNTGGDILDELTKNQOLNE 59
DB 1 MNKNNTYLSRALPSFIDYNGIYGATGATKDTMMI FKTIDYGDILDELTKNQOLND 60
QY 60 ISGLDGVNSLNDLIAQGNLDELSELKEILKANEQKVANDVTKDLAINMLNTYLPK 119
DB 61 ISGLDGVNSLNDLIAQGNLDELSELKEILKANEQKVANDVTKDLAINMLNTYLPK 120
QY 120 ITSMUSDVKNQYALGLQIEYLSKQKIEISDKLDVINNVNLINSTLTETPAYORIKYV 179
DB 121 ITSMUSDVKNQYALGLQIEYLSKQKIEISDKLDVINNVNLINSTLTETPAYORIKYV 180
QY 180 EKPEALTSATETNKTQDSSHTDILDELTELTLASVTKNVDGFEFYLTNTHDVMIG 239
DB 181 EKPEALTSATETNKTQDSSHTDILDELTELTLASVTKNVDGFEFYLTNTHDVMIG 240
QY 240 NNLFGRSALKTASFLIAKENIKTSGSEVGNVNYFLVLTALQAKAFLLTTCRKLGLAD 299
DB 241 NNLFGRSALKTASFLIAKENIKTSGSEVGNVNYFLVLTALQAKAFLLTTCRKLGLAD 300
QY 300 IDYTPINHEHLNKEKEEFVNIPLTSLNTPSNPNYKARGSDKDAKIMEAKPGVALVGF 359
DB 301 IDYTPINHEHLNKEKEEFVNIPLTSLNTPSNPNYKARGSDKDAKIMEAKPGVALVGF 360
QY 360 EISKQSIAYLKQYQAKLKNYQIDKDSLSEIYVGDIDKLCPOSSEQMYTNKIAFPNEY 419
DB 361 EISNDSTYVLKVEAKLKQYQVQDKSLSEVIYSDMDKLCPOSSEQMYTNKIAFPNEY 420
QY 420 VITKIAFTKLNLSRVEYTNFVDSSTGDDIDLNKKKIESSEAEFSMANNNDGYMPTIGT 479
DB 421 VITKIDFTKCKMKTLYRYVLANFYDSSSTGDDIDLNKKKVESSEAEYRTLSANNNDGYMPLGV 480
QY 480 ISETFLTPINGFLVDENSRVLTLCCKSYLRETLATDLSNKEKTLVPPNGFISNIVE 539
DB 481 ISETFLTPINGFLQADENSRVLTLCCKSYLRETLATDLSNKEKTLVPPNGFISNIVE 540
QY 540 NGULEGENLEPMWANNKNAVYDHTGVNGTKVLYHEDGFSQFIDGKDKLKTBYVLYQYI 599
DB 541 NGULEGENLEPMWANNKNAVYDHTGVNGTKVLYHEDGFSQFIDGKDKLKTBYVLYQYI 600
QY 600 VKGKAATYLDKRNQDYIYETNNELDFQAVTKRFTTGDSRVHLIFTSQNGEBAFGG 659
DB 601 VKGKAATYLDKRNQDYIYETNNELDFQAVTKRFTTGDSRVHLIFTSQNGEBAFGG 660
QY 660 NFIISEIRPEELLSPELIKSDAMVGSQGTWISGNSLNINSNVNGTFRONLSLESYSTYS 719
DB 661 NFIISEIRPEELLSPELIKSDAMVGSQGTWISGNSLNINSNVNGTFRONLSLESYSTYS 720
QY 720 MNFNNGFGKVTIRNSREVPERSYLOFSSKXISEKFTTTNNGLYVELSRASSRGVIN 779
DB 721 MNFNNGFGKVTIRNSREVPERSYLOFSSKXISEKFTTTNNGLYVELSRASSRGVIN 780
QY 780 FGDPSIX 786
DB 781 FNFPSIX 787

RESULT 8
US-10-505-315-32
; Sequence 32, Application US/10505315
; Publication No. US20050210545A1
; GENERAL INFORMATION:
; APPLICANT: Syngenta Participations AG
; APPLICANT: Shen, Zhicheng
; APPLICANT: Warren, Gregory
; APPLICANT: Shokkoski, Frank
; APPLICANT: Kramer, Vance
; TITLE OF INVENTION: Novel Vip3 Toxins and Methods of Use
; FILE REFERENCE: 60163PCT
; CURRENT APPLICATION NUMBER: US/10/505,315
; CURRENT FILING DATE: 2004-08-19
```

PRIOR APPLICATION NUMBER: US 60/362250
PRIOR FILING DATE: 2002-03-06
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn version 3.2
SEQ ID NO 32
LENGTH: 788
TYPE: PR
ORGANISM: *Bacillus thuringiensis*
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (1)-(788)
OTHER INFORMATION: Vip3C-12168 toxin
US-10-505-315-32

Query Match 81.2%; Score 3243.5; DB 5; Length 788;
Best Local Similarity 80.9%; Pred. No. 1,6e-190;
Matches 634; Conservative 65; Mismatches 84; Indels 1; Gaps 1;

4 NKKLSVKALPSFIDYNGIYGFATGIDIMNMIFKTNIGDGLTDLDELKNOQLNEISGK 63
5 NTKMARALPSFIDYNGIYGFATGIDIMNMIFKTDGGLTDLDELKNOQLNEISGK 64
6 LDVNGSLNDLIAOGNLTDELTELAKSVTKNDVDFEFYANTFHDVMIKNLP 123
65 LDVNGSLNDLIAOGNLTDELTELAKSVTKNDVDFEFYANTFHDVMIKNLP 124
124 LSDVKNQVYALGLOEYLSKQLEISDKLDVNNVNLINSTLTETTPAYORIKYNEKE 183
125 LSDVKNQVYALGLOEYLSKQLEISDKLDVNNVNLINSTLTETTPAYORIKYNEKE 184
184 ALTSATETNLKTGDSHTDILDELTELAKSVTKNDVDFEFYANTFHDVMIKNLP 243
185 ELTPATETTLKVKDSSPADILDELTELAKSVTKNDVDFEFYANTFHDVMIKNLP 244
244 GRSALKTASELIAKENLKTSGSEVGNNVFLIVLTALQAKAFLTLTTCRKLGLADIDYT 303
245 GRSALKTASELIAKENLKTSGSEVGNNVFLIVLTALQAKAFLTLTTCRKLGLADIDYT 304
304 PTMNEHLNKEKEEFRRVNIPLTSLNTPSNPNYKARGSDAKIMEAKGVALVGEISK 363
305 PTMNEHLNKEKEEFRRVNIPLTSLNTPSNPNYKARGSDAKIMEAKGVALVGEISK 364
364 DSIAVLKVVQAKLKHNYQIDKDSLSSEIYVGDIDKLCPDQSEQMYTNKIAFPNEVITK 423
365 DSITVLKVEAKLKHNYQIDKDSLSSEIYVGDIDKLCPDQSEQMYTNKIAFPNEVITK 424
424 IATFKLASLRYEVTANFYDSTGDI DLNKKKIESSEAEFSLMANNDGVMPIGTISFT 483
425 IDFTKMKTLRYEVTANFYDSTGDI DLNKKKIESSEAEFSLMANNDGVMPIGTISFT 484
484 FLTPINGFLVVDENSRILVTLTCKSYLRRETLATLDSNKEKLIYPPNGFIINYEGL 543
485 FLTPINGFLVVDENSRILVTLTCKSYLRRETLATLDSNKEKLIYPPNGFIINYEGL 544
544 EGENLEPWKANKNKAIVYDHTGCVNGTKVLYVHEDGFSQFIDGDKLKTREYVIOYIVKSK 603
545 EEDNLEPWKANKNKAIVYDHTGCVNGTKVLYVHEDGFSQFIDGDKLKTREYVIOYIVKSK 604
604 AAIYIKDKENGDYIYEBETNNLEDPOAVTKRFITGDSRVAHLITTSONGEBAFGANFI 663
605 PSIHKLKDEVTGYIHEDTNNNLKDYQITLKRFTGTDLKGVYLLIKSQGDGDAWMDKFTI 664
664 SEIRSEELLSPELKSDAMVSGQGTWISGSLNINSNVNGFERQNLGIESYSTYAMFN 723
665 LEIKRAEDLSPELKSDAMVSGQGTWISGSLNINSNVNGFERQNLGIESYSTYAMFN 724
724 VNGFQKVIIRNSREYVFERSYLQFSKYISEKFTTTNNTGLYELSLRAS-SRGYINFGD 782
725 ASGPNVAVIRNSREYVFERSYLQFSKYISEKFTTTNNTGLYELSLRAS-SRGYINFGD 784
783 PSIK 786
785 VSIX 788

RESULT 9
US-10-505-315-2
Sequence 2, Application US/10505315
Publication No. US20050210545A1
GENERAL INFORMATION:
APPLICANT: Syngenta Participations AG
APPLICANT: Shen, Zhicheng
APPLICANT: Warren, Gregory
APPLICANT: Shokoski, Frank
APPLICANT: Kramer, Vance
TITLE OF INVENTION: Novel Vip3 Toxins and Methods of Use
FILE REFERENCE: 60163PCT
CURRENT APPLICATION NUMBER: US/10/505,315
CURRENT FILING DATE: 2004-08-19
PRIOR APPLICATION NUMBER: US 60/362250
PRIOR FILING DATE: 2002-03-06
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 788
TYPE: PR
ORGANISM: *Bacillus thuringiensis*
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (1)-(788)
OTHER INFORMATION: The Xaa at position 738 is either the amino acid Glu or Gly.
US-10-505-315-2

Query Match 81.1%; Score 3239; DB 5; Length 788;
Best Local Similarity 80.7%; Pred. No. 3e-190;
Matches 636; Conservative 64; Mismatches 86; Indels 2; Gaps 2;

1 MOKNN-KLSVKALPSFIDYNGIYGFATGIDIMNMIFKTNIGDGLTDLDELKNOQLNE 59
1 NMKNNTKLSRALPSFIDYNGIYGFATGIDIMNMIFKTDGGLTDLDELKNOQLNE 60
60 ISGKLGVNGSLNDLIAOGNLTDELTELAKSVTKNDVDFEFYANTFHDVMIKNLP 119
61 ISGKLGVNGSLNDLIAOGNLTDELTELAKSVTKNDVDFEFYANTFHDVMIKNLP 120
120 ITSMISDVKNQVYALGLOEYLSKQLEISDKLDVNNVNLINSTLTETTPAYORIKYVN 179
121 ITSMISDVKNQVYALGLOEYLSKQLEISDKLDVNNVNLINSTLTETTPAYORIKYVN 180
180 EKFEALTSATETNLKTGDSHTDILDELTELAKSVTKNDVDFEFYANTFHDVMIKNLP 239
181 EKFEALTSATETNLKTGDSHTDILDELTELAKSVTKNDVDFEFYANTFHDVMIKNLP 240
240 NNLFGRSALKTASELIAKENLKTSGSEVGNNVFLIVLTALQAKAFLTLTTCRKLGLAD 299
241 NNLFGRSALKTASELIAKENLKTSGSEVGNNVFLIVLTALQAKAFLTLTTCRKLGLAD 300
300 IDYPTMNEHLNKEKEEFRRVNIPLTSLNTPSNPNYKARGSDAKIMEAKGVALVGE 359
301 IDYPTMNEHLNKEKEEFRRVNIPLTSLNTPSNPNYKARGSDAKIMEAKGVALVGE 360
360 EISKDSIAVLKVVQAKLKHNYQIDKDSLSSEIYVGDIDKLCPDQSEQMYTNKIAFPNE 419
361 EMSNDSITVLKVEAKLKHNYQIDKDSLSSEIYVGDIDKLCPDQSEQMYTNKIAFPNE 420
420 VITKIDFTKMKTLRYEVTANFYDSTGDI DLNKKKIESSEAEFSLMANNDGVMPIGT 479
421 VITKIDFTKMKTLRYEVTANFYDSTGDI DLNKKKIESSEAEFSLMANNDGVMPIGT 480
480 ISEFTPLINGFLVVDENSRILVTLTCKSYLRRETLATLDSNKEKLIYPPNGFIINYE 539
481 ISEFTPLINGFLVVDENSRILVTLTCKSYLRRETLATLDSNKEKLIYPPNGFIINYE 540
540 NGNLEGENLEPWKANKNKAIVYDHTGCVNGTKVLYVHEDGFSQFIDGDKLKTREYVIOYI 599

Db 541 NGSEEDNEPWRANKNAAYVDHTGVTGKALYHKGDSQFIDGDKPKTEYVIQYT 600
Qy 600 VKGKAAIYLKDEKNGDIYIETNNLEDFQAVTKRFTGTDSRVHLIFTSQGEAFGG 659
Db 601 VKGKPSIHLKDEMTGYIHEDTNNLNKDYOITIKRFTGTDLKGVIILKSONGDEAMGD 660
Qy 660 NFIISIRPEEELISPELLIKSDAMVGSQGTWISGNSLINSNVNGTFRQMLSLSESYTS 719
Db 661 KFTILIKPAEDLLSPBLINPNNSWITTPGASISGNKLPINLGTNGTFRQSLINSYSTYS 720
Qy 720 MNFNVGFGKVTIRNSREVEFSYLOFSKYSISEKFTTTNTNGLYVELSRAS-SRGVI 778
Db 721 ISFTASGPFVTVYRNSRGVLFERSNLMSSHTSHSGFTKESNNTGLYVELSRASGGGCHI 780
Qy 779 NFGDPSIK 786
Db 781 SFENVSIK 788

RESULT 10
US-10-505-315-11
; Sequence 11, Application US/10505315
; Publication No. US20050210545A1
; GENERAL INFORMATION:
; APPLICANT: Syngenta Participations AG
; APPLICANT: Shen, Zhicheng
; APPLICANT: Warren, Gregory
; APPLICANT: Shokoski, Frank
; APPLICANT: Kramer, Vance
; TITLE OF INVENTION: Novel Vip3 Toxins and Methods of Use
; FILE REFERENCE: 60163PCT
; CURRENT APPLICATION NUMBER: US/10/505,315
; CURRENT FILING DATE: 2004-08-19
; PRIOR APPLICATION NUMBER: US 60/362250
; PRIOR FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent version 3.2
; SEQ ID NO 11
; LENGTH: 788
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Hybrid Vip3A-C toxin
US-10-505-315-11

Query Match 81.0%; Score 3235; DB 5; Length 788;
Best Local Similarity 80.5%; Pred. No. 5.3e-190;
Matches 634; Conservative 64; Mismatches 88; Indels 2; Gaps 2;

Qy 1 MOKNN-KLSVKALPSFIYFNGIYGFATGIKOIMNMIKTNNGDGLTDLDELKNOQLNE 59
Db 1 MOKNNKLTSLRALPSFIYFNGIYGFATGIKOIMNMIKTDGADLTDLDELKNOQLND 60
Qy 60 ISGKLDGVNGSLNDLDAQNLDTLSEKELIKIANEQNKVLDVNTKLDALINMLNTYLPK 119
Db 61 ISGKLDGVNGSLNDLDAQNLDTLSEKELIKIANEQNKVLDVNTKLDALINMLNTYLPK 120
Qy 120 TTSMSLDVKNQYALGLQIEYLSKQIKESISDKLDVINNVNLINSTLTETTPAYORIKYVN 179
Db 121 TTSMSLDVKNQYALGLQIEYLSKQIKESISDKLDVINNVNLINSTLTETTPAYORIKYVN 180
Qy 180 EKPEALTSATETMLKTODSSHDTLDELTELTELAKSVTKNVDPDEPEALNPFHVMG 239
Db 181 EKPEELTFPTETISSKVKKQSPADIDDELTELTELAKSVTKNVDPDEPEALNPFHVMG 240
Qy 240 NNLFGRSALKTASSELIAKENLKTSGSEVGAVNPLIVLTLQAKAEFTLTTCRKLGLAD 299
Db 241 NNLFGRSALKTASSELITKENVKTSGSEVGAVNPLIVLTLQAKAEFTLTTCRKLGLAD 300
Qy 300 IDYTPIMNHLNKEKEEPRVNIPTLSNTPSNPNYKARSGDYAKIIMEAKGVYLVGF 359
Db 301 IDYTSIMNHLNKEKEEPRVNIPTLSNTPSNPNYKARSGDYAKIIMEAKGVYLVGF 360

Qy 360 EISKDSIALVLYQVQALKHNYQIDKDSLSIEYVGDIDKLLCPDQSQMYYTINKIAPENEX 419
Db 361 EISNDSITVLKVEALKQNYQYDCKSLSEVYIGDMDKLLCPDQSQIYYTNNIVFPNEX 420
Qy 420 VITKIAFTKLSLRIRYVTPANFDSSTGDIIDLKKKIESSEAFSLNANDGVNPIGT 479
Db 421 VITKIDFTKMKKIRYEVTPANFDSSTGDIIDLKKKVESEAEYRVLISANDGVNPIGV 480
Qy 480 ISFTPLTPINGFGLVYDENSRLVTLCKSYIREFTLATDLSNETKLIYVPPNGPISNIVE 539
Db 481 ISFTPLTPINGFGLQADENSRLITLCKSYIREFTLATDLSNETKLIYVPPNGPISNIVE 540
Qy 540 NGNLBENLEPWRANKNAAYVDHTGVTGKALYHEDGSPQFIDGDKLKTETEVYIQT 599
Db 541 NGSEEDNEPWRANKNAAYVDHTGVTGKALYHKGDSQFIDGDKLPKTEYVIQYT 600
Qy 600 VKGKAAIYLKDEKNGDIYIETNNLEDFQAVTKRFTGTDSRVHLIFTSQGEAFGG 659
Db 601 VKGKPSIHLKDEMTGYIHEDTNNLNKDYOITIKRFTGTDLKGVIILKSONGDEAMGD 660
Qy 660 NFIISIRPEEELISPELLIKSDAMVGSQGTWISGNSLINSNVNGTFRQMLSLSESYTS 719
Db 661 KFTILIKPAEDLLSPBLINPNNSWITTPGASISGNKLPINLGTNGTFRQSLINSYSTYS 720
Qy 720 MNFNVGFGKVTIRNSREVEFSYLOFSKYSISEKFTTTNTNGLYVELSRAS-SRGVI 778
Db 721 ISFTASGPFVTVYRNSRGVLFERSNLMSSHTSHSGFTKESNNTGLYVELSRASGGGCHI 780
Qy 779 NFGDPSIK 786
Db 781 SFENVSIK 788

RESULT 11
US-10-099-285-82
; Sequence 82, Application US/10099285
; Publication No. US20030105319A1
; GENERAL INFORMATION:
; APPLICANT: Schnepf, H. Ernest
; Micker, Carol
; Narva, Kenneth E.
; Walz, Michelle
; Stockhoff, Brian
; Muller-Cohn, Judy
; TITLE OF INVENTION: Toxins Active Against Peets
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: Saliwanichik, Lloyd & Saliwanichik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/099,285
; FILING DATE: 15-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/002,285
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/886,615
; FILING DATE: 1-JUL-1997
; APPLICATION NUMBER: US 08/674,002
; FILING DATE: 1-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: MA-701C2

TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 789 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 82:
US-10-099-285-82

Query Match 79.7%; Score 3182.5; DB 4; Length 789;
Best Local Similarity 79.0%; Pred. No. 8.8e-187;
Matches 624; Conservative 69; Mismatches 92; Indels 5; Gaps 3;

```
QY 1 MOKNN-KLSVKAALPSFDYFNGIYGFATGIKDIMNMI FKTMTGGDLTLDLILKNOQOLINE 59
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
    1 MNKNMFKLSTRALPSFDYFNGIYGFATGIKDIMNMI FKTMTGGDLTLDLILKNOQOLINE 60
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY 60 ISGKLDGVNGSLNDLILKNOQOLINE 119
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
    61 ISGKLDGVNGSLNDLILKNOQOLINE 120
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY 120 ITSMUSDVWKQNYALGLQIEYLSKQLEISDKLDIVNVNVLINSTLTETTPAYORIKYVN 179
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
    121 ITSMUSDVWKQNYALGLQIEYLSKQLEISDKLDIVNVNVLINSTLTETTPAYORIKYVN 180
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY 180 EKFEALTSATETNLTQDSSHTDILDELTELTELAKSVTKNDVDFEFYLTTFHDVMIG 239
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
    181 EKFEALTSATETNLTQDSSHTDILDELTELTELAKSVTKNDVDFEFYLTTFHDVMIG 240
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY 240 NNLFGRSALKTASELAKENLTSGSEVGNVNVNVLVLTALQAKAFITTTCKLIGLAD 299
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
    241 NNLFGRSALKTASELAKENLTSGSEVGNVNVNVLVLTALQAKAFITTTCKLIGLAD 300
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY 300 IDYTPIMNEHLNKEKEEFNVNLTPTLSNTPFSNPNTAKAGSDKAKIIMEAKRGYALVGF 359
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
    301 IDYTPIMNEHLNKEKEEFNVNLTPTLSNTPFSNPNTAKAGSDKAKIIMEAKRGYALVGF 360
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY 360 EISKDSIALVKYQAKLKHNYIDKDSISEIYVGDIDKLCPDQSEQMYTTNKIAFPNEY 419
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
    361 EMSNDSITVLKYEAKLKONYQVDKDSISEVIYGDIDKLCPDQSEQMYTTNKIAFPNEY 420
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY 420 VITTKIAFTKKNLSLAEYLTANFYDSSGTDIDLNKKIISSEAEBSMLAANDGVYMPYGT 479
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
    421 VITTKIAFTKKNLSLAEYLTANFYDSSGTDIDLNKKIISSEAEBSMLAANDGVYMPYGT 480
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY 480 ISETFLTPINGFGLVVDENSRLVTLTKSYLRETLATDLSNKETKLTVPNPGFISNIVE 539
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
    481 ISETFLTPINGFGLVVDENSRLVTLTKSYLRETLATDLSNKETKLTVPNPGFISNIVE 540
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY 540 NGNIEGEMLEPWKANKNAAYDHTGTVGTVLVYHEDGEFSOPIGDKLKTETEVIOYI 599
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
    541 NGNIEGEMLEPWKANKNAAYDHTGTVGTVLVYHEDGEFSOPIGDKLKTETEVIOYI 600
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY 600 VKGAAATYKDEKNGDYIEETNNELEBPQAVTRFRTGTSRSKRVHLIFTSQNGEBAFG 659
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
    601 VKGAAATYKDEKNGDYIEETNNELEBPQAVTRFRTGTSRSKRVHLIFTSQNGEBAFG 660
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY 660 NFIIISIRPSEBELLSPELLIKSDAWVSGQWTISGNSLINSNVNCTPRONLSLSYSTYS 719
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
    661 NFIIISIRPSEBELLSPELLIKSDAWVSGQWTISGNSLINSNVNCTPRONLSLSYSTYS 720
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY 720 MNFVNVNGPKATTINNSREVVFPERSYLOPSSKYISEKPTTTNTNGLVYELSPRASS--RG 776
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
    721 MNFVNVNGPKATTINNSREVVFPERSYLOPSSKYISEKPTTTNTNGLVYELSPRASS--RG 779
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY 777 VINNGDFSIK 786
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
    778 VINNGDFSIK 789
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY 789 IVHFNVDVSIK 789
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
```

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RESULT 12
US-10-099-285-84
Sequence 84, Application US/10099285
Publication No. US20030105319A1
GENERAL INFORMATION:
APPLICANT: Schepf, H. Ernest
Wicker, Carol
Narva, Kenneth E.
Walz, Michelle
Stokhoff, Brian
Muller-Cohn, Judy
TITLE OF INVENTION: Toxins Active Against Pests
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/099,285
FILING DATE: 15-Mar-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/002,285
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/886,615
FILING DATE: 1-JUL-1997
APPLICATION NUMBER: US 08/674,002
FILING DATE: 1-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-701C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 789 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 84:
US-10-099-285-84

Query Match 79.6%; Score 3180.5; DB 4; Length 789;
Best Local Similarity 78.9%; Pred. No. 1.2e-186;
Matches 623; Conservative 70; Mismatches 92; Indels 5; Gaps 3;
```

```
QY 240 NNLFGSALKTASJELAKENLKTSGSEVGVNFFLVLTALQAKAFLLTTCRKLGLAD 239
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 NNLFGSALKTASJELAKENLKTSGSEVGVNFFLVLTALQAKAFLLTTCRKLGLAD 300
QY 300 IDYTPIMNEHLNKEKEEFVNILPTLSNTPSNPNYKARSDKAKIMEAKGYALVGF 359
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 IDYTSIMNEHLNKEKEEFVNILPTLSNTPSNPNYKARSDKAKIMEAKGYALVGF 360
QY 360 EISKDSIAVLKYQALAKHNYQIDKOSLSBIYVGDIDKLCPQOSEQMTYTKIAPFNEY 419
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 361 ESKNSDISIVLKYVEALQKONYQVDKOSLSBIYVGDIDKLCPQOSEQIYYTNNIIVPENEX 420
QY 420 VITKIAFTKKLNSLRREYVTFANFYDSSTGDIIDLNKKKIESSEAFSMLNANDGVNPIGT 479
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 421 VITKIDFTKKMKTLEEVTFANFYDSSTGDIIDLNKKKVESSEAFRTLSANDGVNPIGLV 480
QY 480 ISETFLTPINGFGLVVDENSRLVTLTCKSYLRETLATDLSNKETKLIYPNGFISNIYE 539
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 481 ISETFLTPINGFGLQADGNSRLITLTCCKSYLRETLATDLSNKETKLIYPNGFISNIYE 540
QY 540 NGNLEGENLEPMKANKNAVVDHTGCVNGTKVLYNHEDEFSQFIDGDKLKTREYIYQYI 539
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 541 NGSIEBDNLEPMKANKNAVVDHTGCVNGTKVLYNHDGGSQFIDGDKLPKTEYIYQYT 600
QY 600 VKGKAIIYLKDEKNGDIYIYEETNNELEDFOAVTKRFTGTDSRVHLIFTSQNGEAFGG 659
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 601 VKGKPSIHLKDEMTGYIHEDTNNNLKDQYITTKRFTGTGDLKGVLILKSQNGDEAMGD 660
QY 660 NFIIISIRPSEELLSPELIKSDAWGSOGTWISGNSLINSVNGTFRONSLESYSTYS 719
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 661 NFIIISIRPSEKLLSPELINTNMTSTGTHISGNTLTLVQGGKGLIKQNLQDPSFYR 720
QY 720 MNPNNVGFQKVTIRNSREVVPERSYLOFSSKYSIKETTTTNTGLYELSRASS---RG 776
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 721 VYFVSVDGNAVIRNSREVLFEKGYMS-GAKDVSEMTTTFEKNDFIIELSQGNLYGSP 779
QY 777 VINFGFSIK 786
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 780 IYHFYVSIK 789

RESULT 13
US-10-099-285-92
: Sequence 92, Application US/10099285
: Publication No. US20030105319A1
: GENERAL INFORMATION:
: APPLICANT: Schneck, H. Ernest
: Wicker, Carol
: Narva, Kenneth E.
: Walz, Michelle
: Stockhoff, Brian
: Muller-Cohn, Judy
: TITLE OF INVENTION: Toxins Active Against Peets
: NUMBER OF SEQUENCES: 105
: CORRESPONDENCE ADDRESS:
: ADDRESSER: Saliwanichik, Lloyd & Saliwanichik
: STREET: 2421 N.W. 41st Street, Suite A-1
: CITY: Gainesville
: STATE: Florida
: COUNTRY: USA
: ZIP: 32606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/10/099,285
: FILING DATE: 15-Mar-2002
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 09/002,285
```

```

: FILING DATE: <Unknown>
: APPLICATION NUMBER: US 08/886,615
: FILING DATE: 1-JUL--1997
: APPLICATION NUMBER: US 08/674,002
: FILING DATE: 1-JUL-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Sanders, Jay M.
: REGISTRATION NUMBER: 39,355
: REFERENCE/DOCKET NUMBER: MA-701C2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (352) 375-8100
: TELEFAX: (352) 372-5800
: INFORMATION FOR SEQ ID NO: 92:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 789 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: SEQUENCE DESCRIPTION: SEQ ID NO: 92:
US-10-099-285-92

Query Match 79.5%; Score 3176.5; DB 4; Length 789;
Best Local Similarity 78.9%; Pred. No. 2,1e-186;
Matches 623; Conservative 69; Mismatches 93; Indels 5; Gaps 3;

QY 1 MCKNN-KLSYKALPSTIDYVNGIYGPATGKIDIMNMIFFKTNNGDILTBELIKNOOLNE 59
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MNKNNTKLSARALPSPIDYVNGIYGPATGKIDIMNMIFFKTDGNTLTBELLKNOOLNE 60
QY 60 ISGKLGNGSLNDLLAOGNLTDELSEKELIKANEONKVLNDVNTKLDALINMLNTYLPK 119
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ISGKLGNGSLNDLLAOGNLTDELSEKELIKANEONQVLNDVNNKLDALINMLHYLPK 120
QY 120 ITSMLSDVKNQNYALGLQIEYLSKQKEISDKLDVINNVVLINSTLTETIPAYQRIKYVN 179
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 ITSMLSDVKNQNYALGLQIEYLSKQKEISDKLDVINNVVLINSTLTETIPAYQRIKYVN 180
QY 180 EKFEALTSATETNMLTKQDSSHTDIDDELTELTELAKSVTKNDVDGFEPLANTFHDVMIG 239
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 EKFEALTFATEYTLKVKQSSPADIIDELTELTELAKSVTKNDVDGFEPLANTFHDVMIG 240
QY 240 NNLFGSALKTASJELAKENLKTSGSEVGVNFFLVLTALQAKAFLLTTCRKLGLAD 239
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 NNLFGSALKTASJELAKENLKTSGSEVGVNFFLVLTALQAKAFLLTTCRKLGLAD 300
QY 300 IDYTPIMNEHLNKEKEEFVNILPTLSNTPSNPNYKARSDKAKIMEAKGYALVGF 359
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 IDYTSIMNEHLNKEKEEFVNILPTLSNTPSNPNYKARSDKAKIMEAKGYALVGF 360
QY 360 EISKDSIAVLKYQALAKHNYQIDKOSLSBIYVGDIDKLCPQOSEQMTYTKIAPFNEY 419
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 361 ESKNSDISIVLKYVEALQKONYQVDKOSLSBIYVGDIDKLCPQOSEQIYYTNNIIVPENEX 420
QY 420 VITKIAFTKKLNSLRREYVTFANFYDSSTGDIIDLNKKKIESSEAFSMLNANDGVNPIGT 479
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 421 VITKIDFTKKMKTLEEVTFANFYDSSTGDIIDLNKKKVESSEAFRTLSANDGVNPIGLV 480
QY 480 ISETFLTPINGFGLVVDENSRLVTLTCKSYLRETLATDLSNKETKLIYPNGFISNIYE 539
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 481 ISETFLTPINGFGLQADGNSRLITLTCCKSYLRETLATDLSNKETKLIYPNGFISNIYE 540
QY 540 NGNLEGENLEPMKANKNAVVDHTGCVNGTKVLYNHEDEFSQFIDGDKLKTREYIYQYI 539
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 541 NGSIEBDNLEPMKANKNAVVDHTGCVNGTKVLYNHDGGSQFIDGDKLPKTEYIYQYT 600
QY 600 VKGKAIIYLKDEKNGDIYIYEETNNELEDFOAVTKRFTGTDSRVHLIFTSQNGEAFGG 659
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 601 VKGKPSIHLKDEMTGYIHEDTNNNLKDQYITTKRFTGTGDLKGVLILKSQNGDEAMGD 660
QY 660 NFIIISIRPSEELLSPELIKSDAWGSOGTWISGNSLINSVNGTFRONSLESYSTYS 719
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 661 NFIIISIRPSEKLLSPELINTNMTSTGTHISGNTLTLVQGGKGLIKQNLQDPSFYR 720
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QY	211	-LTEL- -KSVTKNDVDGPEFY-----LTFPHDVMIGNLFGSALKTA	253
Db	246	VINQAAQGVSTTKNALNGENLEBAKQOASQSLGSLDNLNNAOKQVTDIDINGAHVDEA	305
QY	252	SELIAKENKTSGSSEGVNVNPLIVLTALQA-----KAPFLITTT-----	290
Db	306	NGI--KQNGQNTMTANGLKQA LADDA TKA TVTFDADQAKQA VYTA VTNENITSKA	366
QY	291	-----CRKLGLADI DY-----TPIMN- EHIN-----	311
Db	364	NGGNATQAEVEQA IKQVNAKQALNPNANVQAHKDEBATALINSNDLNQA QKDALKQVQ	423
QY	312	-----KEKEFE RVNII LPTLSNTSPENVEKARGS-----DKD-----AK	343
Db	424	NATTVAGVNNVKNQTAOELNANMTQLKQGLADKEQTTADGQFVNADPDKQANVQA VAKAE	483
QY	346	IMEAKPGYALVGFELISKDSIAVLKYYQAQKKNYQIDKQSLSEIYVGIDIKLCPDQSE	405
Db	484	ALISATPDVVVTPSEI---TAALNKVTOAKNDNGMTNLATATQONVQHALIDQLPNLNAQ	540
QY	406	QWYTNKIA-----FPEYVYITKIAFTKK-----LNSLREYVTA NYDSSTDGIDIL	451
Db	541	REYSKQITQATLVPNVNAIQQAATTINDAMTQLKQGIANKQA IKSESYNHADADTKQTA	600
QY	452	NKKKIESSFAEFSMLNANNDBGVYMPITGTSFELPFGNGVLVDNSRLVTLTCSYLR	511
Db	601	YMNATYKAE---ELKQTTNPTMPD-NTIQQA-LTVYNDTQNALNGQKKA--DAKQDAK	653
QY	512	ETLLATLDSNKETKLI V-----PENGFSI NVENGNEGENLEBPWKANNKQA VYDHTG	564
Db	654	TTLGTLHDHNDQKQALTTQVEQAPDIATVNNVKQ----AQNLNNA MTNLNNA LDKTE	709
QY	565	GYN-----GTRKLYV-----HEGGE SQF GDL-KLKTREYVI QY YKGAALY LKD	610
Db	710	TLNSINFTDADQAKDQAYTNAVSHAGILSKANGSNASTREYVQAMQRVNEAKQALNGND	769
QY	611	-----EKQGDVYEERTN--NELEDFQAVT	632
Db	770	NVQRAKDAKQVITNANDLNQAMTQKQGLADKQCTKANGFNPNADTDKQANVNAVAHA	829
QY	633	KRFITGDSRVHLIFTSQ-----NGEENAF-----GQNFISBI-----PSPSE	671
Db	830	EQIISGTFPANDPQQVAQALQOVNAQKAGDLNGNHNLIQVAKONANATIDQLPPLNGPQKT	889
QY	672	LISPELISDANVWSQGTWISGNSLINSNNVNGTFPQNLSLBSYSTYSNMF	722
Db	890	AKQDVSHAEVLTGVNAIKQNDALN--NMGTTLKQOIQANSQVPSVD F	937

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; PRIOR FILING DATE: 2004-09-28
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: Patencin Ver. 3.3
; SEQ ID NO 41
; LENGTH: 2710
; TYPE: PRF
; ORGANISM: Clostridium difficile
US-11-051-453-41

Query Match      4.6%; Score 183; DB 11; Length 2710;
Best Local Similarity 18.5%; Pred. No. 0.043;
Matches 191; Conservative 164; Mismatches 338; Indels 338; Gaps 48;

QY      37 EPTNNGDGLTDELILKNOQLNEISGKLDGVNGSLNDLLAGNTL-----DTE 83
      |||:::| ||||| ||||| ::| ::| ::| ::|
Db      660 FNTISFARLSVD-----SLSNESISFDDTKLDISPRQVEVNLGCMFSDPNVEET 713
QY      84 LSKELKILANEONKVLVDNVTKLDAINMLMTYLPKITS-----ML 124
      |||:::| ||||| ||||| ::| ::| ::| ::|
Db      714 PGKLLLSIMDKITSLPDPVNK--NSITGANQVEVRINSERKELLAHSGWINKERAIM 771
QY      125 SDPMKQNT---ALGLQIEYLSKO---LKEISDKLDVI-----NVNVLINSTLEIT 169
      |||:::| ::| ::| ::| ::| ::| ::| ::|
Db      772 SDSLSEKEYIFPDSDIDNKLKAKSKNIPGLASISSEDIKTLLDASVPTKPFILMLKINIE 831
QY      170 PAYORKIVNKEFELATGATETNLKTQDSSH--TDLDLDELTELKAVTKNDVNGFE 227
      |||:::| ||||| ||||| ||||| ||||| ::|
Db      832 SSGIDYIY--EKLEPVKNIIHNSIDDLIDEFNLLENVSDLEYELKLU-----NNLD--E 882
QY      228 FYLNTFHDVMIQGNLF-----GRSA--LKTASELJAKENLKTSGSEGVNVPFLIV- 276
      |||:::| ||||| ||||| ||||| ||||| ::|
Db      883 KYLSFEDISKNNSTYSVRFINKNGSGSVYETEKEIFSKYSEHIT--KEISTIKNSITTD 941
QY      277 -----LTLQAKAFL-----TLTTCRKL-----LGLA 298
      |||:::| ||||| ||||| ||||| ||||| ||
Db      942 VNGMLDNIQDHTSQVNTLNAAPFISQLIDYSSNKNVDLNDLSYKVOULFYAOLFSTGLN 1001
QY      299 DIDYTPINREHLNKEKEFRVNIPLPTL-----SNTFSNPVY-----EKARGSDQAKI 346
      |||:::| ||||| ||||| ||||| ||||| ||
Db      1002 TI-YDSIQLVNLISNAVNDITINVLPTTBEIPIVSTTLDGINTGAILKELLDHDPILK 1060
QY      347 IMEAKPGYALVGFELSKDS-----IAVLKYVQAKLKNYQIDKDSLS 388
      |||:::| ||||| ||||| ||||| ||||| ||
Db      1061 ELKAKGVGLAINMLSIAATVASIVGIGAEVTIFLPLTLAGISAGISPLVNNELIHDKAT 1120
QY      389 EIV-----YGDV-----DKLCPDQSBQMYTNKIAFPNEYVYTIKIAATKCLNSL 433
      |||:::| ||||| ||||| ||||| ||||| ||
Db      1121 SVVNVFNLSESKYGLPKTEDEDKILVP-----IDDLVISEIDPNV--NSI 1164
QY      434 R-----YEVTAN--FYVS-----STGIDINKKKIES 458
      |||:::| ||||| ||||| ||||| ||||| ||
Db      1165 KLGTGNILNIEGGSGHVTYTGNIHFSPSPSISHPSLSIYSAIGLETENLDFSKIMML 1224
QY      459 SEAEF-----SMLNANDGVMPIGTISE-----TFLTPI- 488
      |||:::| ||||| ||||| ||||| ||||| ||
Db      1225 PNAISRVEFMETGAVPGLRSLENDGRTL--LDSIRDLVPGKFWRFYAFPDYALTTLKPY 1283
QY      489 --NFGVLVDENSGVLTLTKSYTARETLATLDSNKEKTIYPPNGFISNIV-----N 540
      |||:::| ||||| ||||| ||||| ||||| ||
Db      1284 EDTNIIKIKLKDRT-----NFMPTITNEIRNKL.SYSPDAGAGYSILLSSYPISTN 1336
QY      541 GNTEGEMLEPMKANKKAAVVDHNG-----VNGTKVLYVHEDGFSQFI 584
      |||:::| ||||| ||||| ||||| ||||| ||
Db      1337 INLSKDLMLFNIDNEVREISINGTIKKKGLIKDVLASKIDIKAKKILIGNQTIIDSQDI 1396
QY      585 GDK-----LKLKTEYVIQYIVGKA--AIYLKDKNGDGIYEETNNELEDFQAVTKR 634
      |||:::| ||||| ||||| ||||| ||||| ||
Db      1397 DNKORVIFLFCELDDKISLIIENLVAKSVSLLSGKN--YLISMLSTIKINTL---- 1451
QY      635 FIITGDSRRHLLFTSQNGEAAQG-----NFIISEIRPSEEL-----SPEI 677
      |||:::| ||||| ||||| ||||| ||||| ||
Db      1452 ---GLDSKNIAVYTESNNKYVGAIAKTSKQSKIHYKKDSKNILFEYNDSTLEFNSKOF 1508

```

Qy 678 IKSAMVGSQ-----GTWISGNSLN-----INSN--VNGFERONLSSESYTY 718
Db 1509 IAEIDINVEKMDINTITGKYVDNNNTKSIDFISISLVKNOVKNGIYLNESVSYLDF 1568
Qy 719 SMN-----FNVNGFGVITRNSREVEFERSYLOFSSKYISEKFTTTNTNGI-YVELSAS 773
Db 1569 VKNSDGHNTSNFNMFLDN--ISFMWLFEPENINFEIDKXFTLVGKTNIGYVEFICDN 1625
Qy 774 SRGV-INFGDF 783
Db 1626 NKONIDYFGEW 1636

RESULT 3
US-11-087-099-12160
; Sequence 12160, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450) B EP
; CURRENT APPLICATION NUMBER: US/11/087, 099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ. ID NOS: 12464
; SEQ. ID NO 12160
; LENGTH: 1778
; TYPE: PRT
; ORGANISM: *Listeria monocytogenes* EGD-e
US-11-087-099-12160

Query Match 4.4%; Score 175; DB 11; Length 1778;
Best Local Similarity 20.2%; Pred. No. 0.069;
Matches 190; Conservative 140; Mismatches 314; Indels 298; Gaps 50;

Qy 4 NNTLS-VKALPSF--IDYFGIYGRATGIDIMNMKTGTGDLT---LDELTKNQOL 56
Db 487 SNRLSDVSTLTNPSPSLYIN--ISNNVIR--TVGKMTLP,SLKEFYAQNNS 533
Qy 57 LNEIS-----GKLDGVNGSLNDLLAQNLDTLSKEI-----LKIA 92
Db 534 ISDISMTHDMPLAKVDASNNLTINIGTFDNLPGQLDVHSNRITTSYIHLPSLET 593
Qy 93 NEONKVLNDVNT---KLDALIMLNTY-----LPKI-TSMLSDVKKONYALG--- 135
Db 594 NAQTNLTINIGTMDNLPDLTVYNLSFRIPLAPIGDLPNLETLIVSDNNSYLRSGTMD 653
Qy 136 -----IQIEYLS-----KOLKEISDGLDVNNVNLNSTITEIT--PAVORIKYVN 179
Db 654 GVEPLRLIDQNNYLNLTGTGEGNLSISDLTNTLMTLRNNVYIDDISGLSTRLYLN 713
Qy 180 -----EKFPALTSATEYNLKTGODSHTDI--LDELTELTELAKSVTKNDVNGFEFYL 231
Db 714 LDSNKEIDISALSNLTNLOELTLENNKIENTISALSDLENLKNLV--VSKNKI----- 763
Qy 232 TFDVNIIGNNLFGRSALKTASE-----LIAKENLXTSGSEVGNVY 271
Db 764 --IDISPVANMVRGALVTASNGTYTLPTVLSYQSSFTINPVIWYGTCTLLASSIGNSG 821
Qy 272 NF--LIIVTALQAKAPLITTCRKLGLADIDYTPIMENHLNKEEFVNILPTLSNT 338
Db 822 NYDGRKITWNTMTATSSTLF-----NFRRLKGL-----TFSGT 856
Qy 329 FSNPNTEKARGSKDKAKIWEAKRGVALVGFESISKDSIAVLKYQAKLKH----- 378
Db 857 VTPP-YKSA-----AKVTADAEQYTT-IGDTISBEQF--LKOVNNASSSGAPVTSDFAT 906
Qy 379 -----NYQIDKDISISEIYGDIDK-----LLCPDQSBQWYTNKIAFPNRYV 420
Db 907 VVDLNTFGEYEVYLTSEKDGIGQSDSKVIYKVLHGAFAVISADGT-----ISYDGHAT 958
Qy 421 ITKIAFTKGLNS--LRYEYLANFYDSSTGIDILANKKISSSEAEPSMLANNDGYMPT 477
Db 959 ITEKQFLBEDIHASTDIDTALTITNF--STA-VNLNK-----GGDYVALNSENEDGVK--- 1007

Qy 478 GTISETEFLTPINGFGLVVDENSRLVLTCKSYLRETLATDLSNKEKRLIVPMGPI SNI 537
Db 1008 ---AEIVYVVT-----VAKDPAPITIS-----AKITITTDKSKTEA-----AFJDDI 1048
Qy 538 ---VENGNLGENLEPMKANNKAAVYDHT-----GGVNGT-KVLVYHDEGFESQFIG 585
Db 1049 DADTNDGSIYTSNFA--TAVVLDKAGDYTVTLNATNEDGVKATPVEVIVHVGQGERPVITAD 1216
Qy 586 DKL-KLCTEYVIOY--IVKGAALYLODEKNGDYIYETNNELE-DFOAVTKRFTITGDS 641
Db 1101 -KATISTNTAQQYETKAKINETOPFLD-VHASINAPPTAVLESDFETVVKLDVPGTYT 1158
Qy 642 SRVHLIFTSONGEAFGNGFII-----SEIRPSELSPEL--IKSDAMVGSQGTWIS 692
Db 1159 --VTITNEDGGVSAPEKESVIVRKIPAPEITDKEITYPKEDVESAEFLNDIHATIS 1216
Qy 693 GNSLINSVNGTFRONLSSESYTYSMNFRVNG----- 726
Db 1217 DKQVALTSN-----FSTDVNLNKA GDYTVTLNATNEDGVKATPVEVIVHVGQGERPVITAD 1272
Qy 727 -----FGKVTYTRNSREVEFERSYLOFSSKYISEKFTTTTN 761
Db 1273 ATISYDKFANITTEKFLIEDIHATISDQSSVTITSNFQTATN 1314

RESULT 4
US-11-045-004-19
; Sequence 19, Application US/11045004
; Publication No. US20060078901A1
; GENERAL INFORMATION:
; APPLICANT: BUCHRIEGER, CARMEN
; APPLICANT: FRANGIUTI, LIONEL
; APPLICANT: COUVE, ELISABETH
; APPLICANT: RUSNIOT, CHRISTOPHE
; APPLICANT: FSHI, HAFIDA
; APPLICANT: DEHOUX, PIERRE
; APPLICANT: DUSSENGET, OLIVIER
; APPLICANT: CHETOUANT, FARID
; APPLICANT: NEJARI, HAFED
; APPLICANT: GLASER, PHILIPPE
; APPLICANT: KUNST, FRANCK
; APPLICANT: COSSANT, PASCALE
; APPLICANT: DANIELS, JUSTIN
; APPLICANT: GOEBEL, WERNER
; APPLICANT: KREFT, JURGEN
; APPLICANT: KUHN, MICHAEL
; APPLICANT: VAQUEZ-BOLAND, ANTONIO
; APPLICANT: DOMINGUEZ-BERNAL, GUSTAVO
; APPLICANT: GARRIDO-GARCIA, PATRICIA
; APPLICANT: TIERREZ-MARTINEZ, ALBERTO
; APPLICANT: AMEND, ALEXANDRA
; APPLICANT: CHAKRABORTY, TRINAD
; APPLICANT: DOMANN, EUGEN
; APPLICANT: HAIN, THORSTEN
; APPLICANT: BERGE, PATRICK
; APPLICANT: CHARBIT, ALAIN
; APPLICANT: DURANT, LIONEL
; APPLICANT: PEREZ-DIAZ, JOSE-CLAUDIO
; APPLICANT: BAQUERO, FERNANDO
; APPLICANT: GARCIA DEL PORTILLO, FRANCISCO
; APPLICANT: GOMEZ-LOPEZ, NURIA
; APPLICANT: MADUENIO, ENCARN
; APPLICANT: PABLOS, BETRIZ DE
; APPLICANT: WEHLAND, JURGEN
; APPLICANT: KARST, UWE
; APPLICANT: ERTIAN, KARL-DIETER
; APPLICANT: HAUF, JORG
; APPLICANT: ROSE, MATTHIAS
; APPLICANT: VOSS, HAMUT
; TITLE OF INVENTION: *Listeria monocytogenes* genome, polypeptides and uses
; FILE REFERENCE: 05394.0018-02

```
/ CURRENT APPLICATION NUMBER: US/11/045,004
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: 10/637,657
/ PRIOR FILING DATE: 2003-08-11
/ PRIOR APPLICATION NUMBER: 10/257,023
/ PRIOR FILING DATE: 2002-10-08
/ PRIOR APPLICATION NUMBER: PCT/FR01/01118
/ PRIOR FILING DATE: 2001-04-11
/ PRIOR APPLICATION NUMBER: FR 00/04,629
/ PRIOR FILING DATE: 2000-04-11
/ NUMBER OF SEQ ID NOS: 2854
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 19
/ LENGTH: 1778
/ TYPE: PR1
/ ORGANISM: Listeria monocytogenes
US-11-045-004-19

Query Match      4.4%; Score 175; DB 11; Length 1778;
Best Local Similarity 20.2%; Pred. No. 0.069;
Matches 190; Conservative 140; Mismatches 314; Indels 298; Gaps 50;

QY      4 NNNLS-VKALPSF--IDYFGIYGATGIDIMMFKTNGGDLT---LDELKKNQOL 56
      487 SNRLSDVSTLTNPSPSLYN--ISNNVIR--TVGKMTLPKELKEFYAQNNS 533
QY      57 LNEIS-----GKLDGVNGSLNDLAAQNLDTLSKEI-----LKIA 92
      534 ISDISMIDHMPNARKYDASNNLITNGTPNLPKQSLDVHSNRITSTSVIHLPBLET 593
QY      93 NEBNKLANDVNT---KLDALNLMNTY-----LPKI-TSMUSDVKNQNYALG--- 135
      594 NAGTNLITNGIDMNPDLTYVNLSEFNRLPSLAPIGDLPLETLIVSDNNSYKRSIGTMD 653
QY      136 -----LQIEYLS-----KQLEISDKLDVINNVNLINSTLEIT--PAQRKKNV 179
      654 GVPKAILDLQNNYNTYGTGEGNLSLSDLTNLTENNNYITIDISGLSTSLRIYLN 713
QY      180 -----EKEEALTSATEYNLKTQDSSTHD1--LDELTELTELAKSVTKNDVDFEFLYN 231
      714 LBSNKLIEDISALSNLTNLQELTLENNKIENISALSLEMLNKLTV--VSKNKI----- 763
QY      232 TRHDWIGNNLFGKRSALKTASF-----LIAXENLKTSGSEVGNVY 271
      764 --IDISPVANMVRKGAIVTASNOTYTLPTVLSYQSSFTIDNPYIWDGTLAPSSIGNSG 821
QY      272 NF---LIIVTALQAKAFLLTTCRKULGLADIDYITNMENHKNKEEPRVNLPLSLNT 328
      822 NYKDGKITTNMTATSSSTLP-----NENRLKQGL-----TFSGT 856
QY      329 FSNPNYEKARGSDKAKIMEAKPGYALVFEISKDSIALVKYQAKLKH----- 378
      857 VTQP-YKSA-----AKVTADAAQTYT-IGDPTISEQF--LKDYNKSSDGAPEYSDPAT 906
QY      379 -----NYQIDKDSLEIVYGDIX-----LICPDQSEQMYTINKIAPENEVY 420
      907 VVDLNTFGEYEVLTSEKDGIOGDSCKYVVKVLHGAPVISAQT-----ISYDKHAT 958
QY      421 ITRKIAFTKILNS---LRYEVTANFYOSSTGDDIDLNKKKISESEAEPSMLNANDGYMYMI 477
      959 IIEKQPLEDIIHASTDIDTAITTF--STA-VNLNK-----GGDYVALNSEDMDGK-- 1007
QY      478 GTISETEFLPPIFGVLVDENSRLLVLTCKSYLRETLATDLSNKEKTLIVPENGISAI 537
      1008 ---AETVYVTVT---VNKDPAIIS-----AKTEIYIDKPSKTEA-----AFLDI 1048
QY      538 ---VENGNLEGNLEWKAANKKAAVYDRT-----GGVNGT-KVLVYHEDGESQFTG 585
      1049 DADTNDGSLVTSNFA--TAVNLDKAGDYTVTLINSINSDVAGTPPAIIYHVEKE----- 1100
QY      586 DKL-KLKTETVLYOY--IVYKGAAYLKDEKNGDYIYEETNNLE--DFQAVTRKRFITGDS 641
      1101 -KIATISTTAOQYEEKYAKINETOFLKD--VHASINASPPTAVLESDFETVVLADVPGYIT 1158
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QY      642 SRVHLIFTSONGEBAFGNFI-----SEIRPSEBLLSPHL--IKSDAMVGSQGTWIS 692
      1159 --VTIATNEDGVSAPKREVSIVYKRIPEPTEADKEITYPKDEVSEAEFLANDIATIS 1216
QY      693 GNSLINSNVNNGTFRONLSLESYSTYSMNPNVG----- 726
      1217 DKVVAITSN---FSTDVNLNKGADYTVTLNMTNEDGVKATPEVIVHVQGERPVITAD 1272
QY      727 -----FGKYTRNSREVVNPFERSYIQFSSKYSIEKFTTTN 761
      1273 ATISYDKFANITFAKFLDIIHATSSDQSSVTYTSNFOTATN 1314

RESULT 5
US-11-045-004-41
/ Sequence 41, Application US/11045004
/ Publication No. US20060078901A1
/ GENERAL INFORMATION:
/ APPLICANT: BUCHRIESER, CARMEN
/ APPLICANT: FRANGEUL, LIONEL
/ APPLICANT: COUVE, ELISABETH
/ APPLICANT: KUSNIOK, CHRISTOPHE
/ APPLICANT: FSIHL, HAFIDA
/ APPLICANT: DEHOUX, PIERRE
/ APPLICANT: DUSURGERT, OLIVIER
/ APPLICANT: CHETOUANI, FARID
/ APPLICANT: MEDJARI, HAPPE
/ APPLICANT: GLASER, PHILIPPE
/ APPLICANT: KUNST, FRANCK
/ APPLICANT: COSSART, PASCALE
/ APPLICANT: DANIELS, JUSTIN
/ APPLICANT: GOEBEL, WERNER
/ APPLICANT: KREFT, JURGEN
/ APPLICANT: KUHN, MICHAEL
/ APPLICANT: NG, EVA
/ APPLICANT: VAZQUEZ-BOLAND, ANTONIO
/ APPLICANT: DOMINGUEZ-BERNAL, GUSTAVO
/ APPLICANT: GARRIDO-GARCIA, PATRICIA
/ APPLICANT: TIERREZ-MARTINEZ, ALBERTO
/ APPLICANT: AMEND, ALEXANDRA
/ APPLICANT: CHAKRABORTY, TRINAD
/ APPLICANT: DOMANN, EUGEN
/ APPLICANT: HAIN, THORSTEN
/ APPLICANT: BERGE, PATRICK
/ APPLICANT: CHARBIT, ALAIN
/ APPLICANT: DURANT, LIONEL
/ APPLICANT: PEREZ-DIAZ, JOSE-CLAUDIO
/ APPLICANT: BAQUERO, FERNANDO
/ APPLICANT: GARCIA DEL PORTILLO, FRANCISCO
/ APPLICANT: GOMEZ-LOPEZ, NURIA
/ APPLICANT: MADUENIO, ENCARN
/ APPLICANT: PABLOS, BETRIZ DE
/ APPLICANT: WEHLAND, JURGEN
/ APPLICANT: KARST, UWE
/ APPLICANT: ENTIAN, KARL-DIETER
/ APPLICANT: HAUF, JORG
/ APPLICANT: ROSE, MATTHIAS
/ APPLICANT: VOSS, HAMOTI
/ TITLE OF INVENTION: LISTERIA MONOCYTOGENES GENOME, POLYPEPTIDES AND USES
/ FILE REFERENCE: 05394,0018-02
/ CURRENT APPLICATION NUMBER: US/11/045,004
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: 10/637,657
/ PRIOR FILING DATE: 2003-08-11
/ PRIOR APPLICATION NUMBER: 10/257,023
/ PRIOR FILING DATE: 2002-10-08
/ PRIOR APPLICATION NUMBER: PCT/FR01/01118
/ PRIOR FILING DATE: 2001-04-11
/ PRIOR APPLICATION NUMBER: FR 00/04,629
/ NUMBER OF SEQ ID NOS: 2854
/ SOFTWARE: PatentIn version 3.3
```

SEQ ID NO 41
 LENGTH: 832
 TYPE: PR
 ORGANISM: Listeria monocytogenes
 US-11-045-004-41

Query Match 4.4%; Score 174; DB 11; Length 832;
 Best Local Similarity 21.2%; Pred. No. 0.028;
 Matches 157; Conservative 113; Mismatches 269; Indels 202; Gaps 36;

QY 133 ALGQIEYLSKQKLEISDKLDVINNVNVLINSTLEIT-----PAYORIKYVNE 180
 DB 9 SLALCFISVSPSLVASADTITAVOITKEATDTTEPTIDOPSRMNSQTPAQKWTASS 68
 QY 181 KFEALTSATE-----TNLTKKODSSHTDIDELTELTELAKSVTKVDVDFEETLWTH 234
 DB 69 BEAATVNSTEENTPKNNLKSTISNSKT--YAEIAPPDVNAKTIANK-ISTE----- 118
 QY 235 DVMIGNNLFGRSALKTASELIKENLKTSGSEGVGVNFIIVLTALQAKAFELTTCRKL 294
 DB 119 DI---NAVSEAELOITNLVATNONTIS-----LTGIEHL 151
 QY 295 LGLADIDYTPIMNEHLNKEEFVNILPTLSNTPSNPNYKANGSDKAKIMEANP-- 352
 DB 152 TALENIN---VNNNELTTIDELFNI---PTLKSISANN--KITGNFSLVKTLPFLHTLE 203
 QY 353 --GYALVGFEL-SKDSIAVLKVYQAKLKHVQIDKDSLE-----IYYGIDK 397
 DB 204 VLGAATLELDLENOPNLVTLSADELEK--KLTKNLSQNLGRIASSISIDWGLS 260
 QY 398 LACPDSQMYTYTKIAFPNNEYITKIAFTKQNSLRYEVANFYDSSGTGIDLNK---- 453
 DB 261 VTLMNLE-----IISVDISGATIDSD--DIHLENPAV 292
 QY 454 KTESSEAEFSMLNANDGYMPTIGTSEFLTPINGGLVVD--ENSRLVTLTCKSYLR 511
 DB 293 KNLDISSNELTRLPKIND--FPL-----LTTINVSNNKIDRLSSKLVDPKLTATLN 342
 QY 512 ETLATLDSNKETLIYPPNGFISNIYENGLEBENLEPKANKANKAYVH-----TGV 566
 DB 343 ADKQAVTLS-----FTIANGNTIIPNVE--NLAAQMYTPKLIISNGTSDQSIMASGEL 396
 QY 567 NG-TKVLVYHED-----GEFSQFIGDKLKTKEVVIQYIVGKAAIY---LKDEK- 612
 DB 397 SGLSKSVTFDEVINSPAIAGKTGYTNOPIEVK---AVPIYADKSVSYAPVNADEAT 453
 QY 613 -----NGDYIEETNNELEDFQAVTKRPTGTSSRVHL-----I 647
 DB 454 FLQDIRASASENAQITSDY-----SEVDPATPGDYTVTLHAKNEFDLKADPVTVVVHI 507
 QY 648 FTSGNGSEAFGNGFIIEIRSEBELLSPELL-KEDANVG--SGGTWISGNSLNNNN 703
 DB 508 NDIOKPPVAVANSNDISFEV--GTELTSEBVLLAKSGAVVTDLYDAIKMEVDLSEVDSKL 565
 QY 704 GTFRONLSLSYSTYS-----MNFNVNFGKVTIR--NSREVAFRSYLOFSKTISEKT 757
 DB 566 GTREATIIAASKGASSDPTKLAVKIYDTEKPIIQINNPBIIHKSGELBGQIIDQVI 625
 QY 758 TTTNN---TGLVVELSRASS 774
 DB 626 TATDNYDQDLNIMHDLKSKVDI 646

RESULT 6
 US-10-878-556A-169
 ; Sequence 169, Application US/10878556A
 ; Publication No. US20050266399A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hoffmann, La-Roche Inc.
 ; TITLE OF INVENTION: HCV regulated protein expression
 ; FILE REFERENCE: 21762
 ; CURRENT APPLICATION NUMBER: US/10/878,556A
 ; CURRENT FILING DATE: 2004-06-28

NUMBER OF SEQ ID NOS: 199
 SOFTWARE: Patentin version 3.1
 SEQ ID NO 169
 LENGTH: 1404
 TYPE: PR
 ORGANISM: Homo sapiens
 PUBLICATION INFORMATION:
 DATABASE ACCESSION NUMBER: humanGP/chr12-q14221
 DATABASE ENTRY DATE: 2003-04-22
 US-10-878-556A-169

Query Match 4.2%; Score 168.5; DB 9; Length 1404;
 Best Local Similarity 21.3%; Pred. No. 0.12;
 Matches 146; Conservative 111; Mismatches 272; Indels 157; Gaps 29;

QY 31 DINAMIKTYMGDGLTDEILIKNOQLINEISGKLDYNGSLINDILAO-GNIDTELS--KE 87
 DB 657 DLQNH-----DTAQNALQDKQOEINIKITTDQVTAQLQDKQEHCSQLESILKEYKE 709
 QY 88 ILKIANQNVYNDVNTKLDALINMLNTYLPKITSMLSDVMKQVYALGLOIEVLSKL-- 145
 DB 710 KYLSLEQTELEBQIKRLPADSLVRAKQALQDQQORQLNTDLELRATELSKQLEM 769
 QY 146 -KEI--SDKLDVINNVNVLINSTLEITPAYORIKYVNEKEEALTSATETMLTKODSSHT 202
 DB 770 EKELVSTRDLQKKSALASIKQKLTQEBEKKILKQDETSLSQETKI-----QHE 821
 QY 203 DILDEL-TELTELAKSVTKVDVDFEETLTFHDVIMGNLFGRSALKTASELIKENL 261
 DB 822 ELNNRIQTYVTELOK--VKMEKELMTSLTVKDKLSKVS---DSLKNSKSEFEKENOK 875
 QY 262 TSGSEGVNPNFIVLTALQAKAFELT--TCRKLGLADIDYTPIMNEHLNKEEFVN 320
 DB 876 GKA-----ALDLEKCKELK-----HOLQOVMENTLKQKELKKS 911
 QY 321 ILPTLSNTPSNPNYKANGSDKAKIMEAPGVALVGFESKDSIAVLKVYQAKLKHNY 380
 DB 912 L-----EKEKASHQKL-----ELNSQEBOLQA-QVTLKONE 944
 QY 381 QIDKDSLEIYVGIDIDKLCPPDSQMYTYTKIAFPNNEYITKIAFTKQNSLRYEVAN 440
 DB 945 KEEQQ-----LOGNINEL--KOSSEQKKQIEALQELKIAVLQTELENKLOQOQLT-- 994
 QY 441 FYDSSGTIDILANKKLESSEAEFSMLNANDGYMPTIGTSEFLTPINGGLVVDENSR 500
 DB 995 ---QAAQELAAEKI-----SVLQNNYE-----KSQETFKLOQSPF----- 1028
 QY 501 LVTLTCKSYLRET-LIAT--DLNKEETKLIYPPNGFISNIYENGLEBENLEPKANKANN 557
 DB 1029 -----YGRSEELATRDOLKSVEKLSLAQEDLISNNQOIGN-QNKLIQELKTAKAT 1079
 QY 558 AYYDHGTGVNGTVLVYHEDSEFSQIGDKLKTKEVVIQYIVGKAA---IYLKDEKN 613
 DB 1080 LEQD-----SAKKEQQLQERCKALQDQKESLKEKELVN--EKSKLAEIIEIKRQEKE 1132
 QY 614 GDYIEETNNELEDFQAVTKRPTGTSSRVHLI-----FTSGNGSEAFGNGFI 661
 DB 1133 ---ITKNEELKSHKLESIKETITNLKDAQQLIIQKLELQGRADSLKAIVAEQEKRNQOI 1188
 QY 662 IIEIRPSEELSPELLKSDANVGSQ 687
 DB 1189 LKQVQKKEBEELKKEPTEKAKLHSE 1214

RESULT 7
 US-11-045-004-1251
 ; Sequence 1251, Application US/11045004
 ; Publication No. US20060078901A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BUCHRIEUSER, CARMEN
 ; APPLICANT: FRANGEUL, LIONEL
 ; APPLICANT: COUVE, ELISABETH
 ; APPLICANT: RUSNIOK, CHRISTOPHE

```

1  APPLICANT: FSIH, HAFIDA
2  APPLICANT: DEHOUX, PIERRE
3  APPLICANT: DUSSEURGET, OLIVIER
4  APPLICANT: CHEUOUANI, FARID
5  APPLICANT: NEDJARI, HAFED
6  APPLICANT: GLASER, PHILIPPE
7  APPLICANT: KUNST, FRANCK
8  APPLICANT: COSSART, PASCALE
9  APPLICANT: DANIELS, JUSTIN
10 APPLICANT: GOEBEL, WERNER
11 APPLICANT: KREFT, JURGEN
12 APPLICANT: KUHN, MICHAEL
13 APPLICANT: NG, EVA
14 APPLICANT: VAZQUEZ-BOLAND, ANTONIO
15 APPLICANT: DOMINGUEZ-BERNAL, GUSTAVO
16 APPLICANT: GARRIDO-GARCIA, PATRICIA
17 APPLICANT: TIERREZ-MARTINEZ, ALBERTO
18 APPLICANT: AMEND, ALEXANDRA
19 APPLICANT: CHAKRABORTY, TRINAD
20 APPLICANT: DOMANN, EUGEN
21 APPLICANT: HAIN, THORSTEN
22 APPLICANT: BERCHE, PATRICK
23 APPLICANT: CHARBIT, ALAIN
24 APPLICANT: DURANT, LIONEL
25 APPLICANT: PEREZ-DIAZ, JOSE-CLAUDIO
26 APPLICANT: BAQUERO, FERNANDO
27 APPLICANT: GARCIA DEL PORTILLO, FRANCISCO
28 APPLICANT: GOMEZ-LOPEZ, NURIA
29 APPLICANT: MADUENIO, ENCARNIA
30 APPLICANT: PABLOS, BETRIZ DE
31 APPLICANT: WEHLAND, JURGEN
32 APPLICANT: KARST, UWE
33 APPLICANT: ENTIAN, KARL-DIETER
34 APPLICANT: HAUP, JORG
35 APPLICANT: ROSE, MATTHIAS
36 APPLICANT: VOSS, HAMUT
37
38 TITLE OF INVENTION: LISTERIA MONOCYTOGENES GENOME, POLYPEPTIDES AND USES
39
40 FILE REFERENCE: 05394.0018-02
41 CURRENT APPLICATION NUMBER: US/11/045,004
42 CURRENT FILING DATE: 2005-01-28
43 PRIOR APPLICATION NUMBER: 10/637,657
44 PRIOR FILING DATE: 2003-08-11
45 PRIOR APPLICATION NUMBER: 10/257,023
46 PRIOR FILING DATE: 2002-10-08
47 PRIOR APPLICATION NUMBER: PCT/FR01/01118
48 PRIOR FILING DATE: 2001-04-11
49 PRIOR APPLICATION NUMBER: FR 00/04,629
50 PRIOR FILING DATE: 2000-04-11
51 NUMBER OF SEQ ID NOS: 2854
52 SOFTWARE: PatentIn version 3.3
53 SEQ ID NO 1251
54
55 LENGTH: 896
56
57 TYPE: PRT
58
59 ORGANISM: Listeria monocytogenes
60
61 US-11-045-004-1251

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[illegible]

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RESULT 8
US-10-909-769-24
: Sequence 24, Application US/10909765
: Publication No. US20060024331A1
: GENERAL INFORMATION:
: APPLICANT: Fernandez-Salas, Ester
: APPLICANT: Steward, Lance E.
: APPLICANT: Lin, Wei-Jen
: APPLICANT: Aoki, Kei Roger
: APPLICANT: Sachs, George
: TITLE OF INVENTION: Toxin Compounds with Enhanced Membrane Translocation Characteristics
: PRT REFERENCE: ALLE0010-100 (WO12003-146)
: CURRENT APPLICATION NUMBER: US/10/909,769
: CURRENT FILING DATE: 2004-08-02
: NUMBER OF SEQ ID NOS: 34
: SOFTWARE: PatentIn version 3.3
: SEQ ID NO 24
: LENGTH: 834
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Amino acid sequence of HC
US-10-909-769-24

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Query Match      4.2%  Score 166.5:  DB 11;  Length 896;
Best Local Similarity 20.1%  Pred. No. 0.082;
Matches 129;  Conservative 106;  Mismatches 224;  Indels 183;  Gaps 31

QY      27  TGKIDNNMIFK--TNTGGDLTLDEI-----LKNQ-QILNIESGKLDSGVNSLNDLLAQ  77
Db      156  SGATTIVNQISEFVGTVSKALIEPFRKAGIDLENBLPTIRLTKRVQGYDALPELKKM  215

QY      78  GNDLDELSELKELIANEQNKYLVNVTGLDAIN-----LMLNTYLPKITSLSVKKON  131
Db      216  GAEAVKTIAPKIPELCAKANQVV-EINEXI PELNKATENVLLVEOQLPKRIDQGOIILVQ  274

QY      132  YALGQLEIYLSKQLEISDKLDVI--NNNVLIN-----STLTETIPAYORIKY---  177
Db      275  KKIP-EIKQIASVSEVDENFGLIKCTYVNDVAVNESGRALDIVIDTMAAIPYIEKIAQNGS  333

QY      178  -----VNEKFAELTSATETNLTKTKODSSHITLIDELTS-----LTE  213

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Query Match	4.1%	Score 163.5	DB 9	Length 834
Beet Local Similarity	19.7%	Pred. No. 0.11		
Matches 170	Conservative 114	Mismatches 274	Indels 305	Gaps 38
Oy	16	IDYENGXYGAFATGDKIDNM-----IFKTNMGDLTLDLKKNOQLNE	59	
Db	126	LGYNKNTYTFPLPSLAEKYNKGVOAGLFLMANEVEDEFTTIMKKDILDKISDVSVILPY	185	
Oy	60	ISGULD-----GVNGSLNDLLAQNL-----TELSKEILKI-----ANEQKYLNDVN	103	
Db	186	IGPALINIGNSALRNENFQAFATAGVAFLEBGFPEFTIPALGVTFEYSSIQREKIKITIE	245	
Oy	104	TKL-----DAINLMINTLPIKITSLSGIVMKONALGQIEISLQLEISDKLVI	155	
Db	246	NCEQRKYRKMDISQNMVSNWLSKITTOFHNINQM-----DLSLQADAIKAKIDL-	298	
Oy	156	NNVNLINSTLEITPAVORIKYVKEFEALTSATETNLKTKQDSHTDILDELTE-----	210	


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Db 476 DKVL-----XIKENSNVITISOKVTVASQITKDGVEVFNSLSISKEYI-- 522
Qy 452 NKKIESSEAFSMLNANDGVYWPICGTI-----SETLTPINGGLV 494
Db 523 -----IEMELLVDGKAVTDGWFYISTTLAKPTIBELNLSYSTDKGEFVASPVN---L 574
Qy 495 VDENSRLVTLTKCSYLAETLLATDLSNKEKTLVPPNGFISNIYENGNGENLEPWKAN 554
Db 575 VDRDEISITSIRYAVLEDDYKVGNSNAKEYASVVDANQKKTAVKVRITVDMN-----D 628
Qy 555 NKRAYVHTGAVGTATLYVHEDESEQFIDKLLKTEYVIQIYKGAAT----- 606
Db 629 GNVIFGVYISGNNGQSDYTPATPASNSVVGKTKTPVEFSLKEAEQDKLTIVYEVDAD 688
Qy 607 -----YLDEKNGDYIYEITNLEDFQAVTKRFTI-----GTDSSRVHL 646
Db 689 NTLLFDVLTHPTLKLKYSDAQGY-----SGNPVATVDLTCKSDITNLEDFDGESEAYYV 744
Qy 647 IFTSQNGEAFGGNFIISE-IRPSEELLSPELIKSDAMVGSOGTWISGNSLANSVNGT 705
Db 745 VWTGSYNLDDGAGIMVDELIGOSSVPRTEITK-----VNAS 782
Qy 706 FRONLSIESYTSYMANNNV-GFCKTIRNSREVFEKRSYLOPSKYS-----EKF 756
Db 783 F-----SLDSVDYTKVALNVLKLSDAVNLANDANKIYEKK-----TNLTKTVPLHGFEL 834
Qy 757 TTTTNNGLYELS 770
Db 835 MSDSGNSYLFENIS 848
```

```
RESULT 10
US-10-793-626-1780
; Sequence 1780, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMBERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P03480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 1780
; LENGTH: 1155
; TYPE: PRN
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1780
```

```
Query Match 4.0%; Score 161.5; DB 9; Length 1155;
Best Local Similarity 18.5%; Pred. No. 0.22;
Matches 170; Conservative 136; Mismatches 285; Indels 327; Gaps 46;
Qy 47 LDEILNQQQLNIEISGKLDGVNSLNDLLAQLDTELK-----ELKLANEQ 95
Db 309 INEATIAELKCKDFSPDYGVDPPL-----ALNTSQSKNSPKKASPRMIMLSIAAEP 361
Qy 96 NKLVNDVNTKLDALINMLNTYLPKITSMLSDV-----MKORYAL----- 134
Db 362 NSGKN-VNKKVKTITNTLS--LNKSNHANNVYWPISNQFUKANYELDDISKEGDTT 418
Qy 135 -----GLQIEYLSKQLKEISDKLDVINNVNLINSTLTETPAYGRIKYNEKFEA 184
Db 419 IKYGYIRPGLELPAIKTQLR---SKDGSIVANGVYDKTYN--TTTYFTYVV--DQYON 472
Qy 185 LMSATETNKTQDSSHHTIIDLTELTLBLAKSVTKND--VGFEPYALTFHDVMIAGNNL 242
```

```
Db 473 ITGSPDLIATPKKETAIKDNQNYPMEVN--IANEVKKDFIVD-----YGNK- 517
Qy 243 FGRSALKTASELAKENMLKTSSEGVGNVNFILVTLAQAKAELTLTKKLLGLADIDY 302
Db 518 -----KON--TTTAAVANVDN----- 531
Qy 303 TPIINHELNKEKEEFVNILPFLSNTPSNPNYKAKGSDAKIIMEAKGYALVGEFIS 362
Db 532 --VNNH-----NEVVYLNQNNQNPKAKYISTYKNGFET---PGEVKV--YEYI 574
Qy 363 KDSIAVLKTYQAALKENYQIDKDSLEIYGGIDKLLCPDQSEOMYTYNKLAPNEYVIT 422
Db 575 -DTNANVDSF-----NPDLSNSVADVTISQFTPKVASADGTRVDINFARSMANGKKYIVT 627
Qy 423 KLAFTKKLSLRYEV-----TANFY-----DST-----GD----- 448
Db 628 QAVRPFGTGVNTEYWLTRDGTNTNDFRGTKSTTVTYLNGSSTAQGNPTYSLADYVW 687
Qy 449 IDLNKKKI-----ESSEAFSMLNANDGVY-----MPIGTISEFTLPPI 488
Db 688 LDKNKGVODDDEKGLAGYVTLKDSNRELQKRVTTDQSGHQFDNLQNGTYTVERAID 747
Qy 489 NGFGLVDENSRLVTLTKCSYLAETLLATDLSNKEKTLVPPNGFISNIYENGNGLE-GEN 547
Db 748 N-----YTPSPANNSTNDALDSDGERDGRKVVAKGTINN--ADNMTVDYGFY 794
Qy 548 LEP-----WKANNKANVY--DHGCVNGTVLYVHEGEF-----SOPFGNK 587
Db 795 LTPKTVNGDYVEDTKDGIQDDNEKGISNVKTVLKNKKGDTTGTITDSNGKYEFTGLE 854
Qy 588 LKLTKEYVIQYIVK-----GKAIFYLDEKN----- 613
Db 855 ---NGDYTFEFEPBEGYPTTKQNSGDEBKDNGKTYTVVADANKTIDSGFYKPIYVL 911
Qy 614 GDYIYEITNNELEDFQAVTKRFTGT-----DSSRVHLFTSQNGEAF---GNGFI 662
Db 912 GDYVEDTK--DGIDQDEKGISGVKTVLKDKNGNAIGTTTDSAGHQFGLNGESYT 969
Qy 663 ISEIRPSEELLSPELIKSDAMVGSOGTWISGNSLANSVNGTFRONLSLE--YST--Y 718
Db 970 VEEETPSG--YTPYANS-----GQDITVDSNGITTTGIINA--DNLITDSGFYKTPKY 1020
Qy 719 SM-----NFWNGFG--KYTIRNSREVFEKRSYLOPSKYSISEKFTTTNN 762
Db 1021 SVGDYVEDTKNDGIQDDNEKGISGVKTVLKDKNKIIS-----TTTDE 1065
Qy 763 TGLYELSPASSRGVINF 780
Db 1066 NCKYQFDNLDSGNVYIIHF 1083
```

```
RESULT 11
US-11-079-463-5584
; Sequence 5584, Application US/11079463
; Publication No. US20060073161A1
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTERIOIDES FR
; FILE REFERENCE: P03480US
; CURRENT APPLICATION NUMBER: US/11/079,463
; CURRENT FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/128,705
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/540,209
; NUMBER OF SEQ ID NOS: 10444
; SEQ ID NO 5584
; LENGTH: 1249
; TYPE: PRN
; ORGANISM: B. fragilis
US-11-079-463-5584
```


Qy 367 AVLK-----VYQAKLKNYQIDK--DSLSEIV-----YGDID 396
Db 4541 NQADEGSALEHIADELPRAKIDANQMIOQKVEDINHLSQNPUNLSNEKNKLIQSIN 4600
Qy 397 KLLPDSQOMYTNKIAFPNEVYTK---IATFKLINSRYE-----436
Db 4601 KLVGINKNEIOQAINKQOIEEN--ATTKIDEVIEETTKLIIAKAEKQVKELSQKRDPAI 4658
Qy 437 -----VTANFYDSNGDIDLMKK-----KIESSEAFSMLNANNQGVMPICITSETFLTP 487
Db 4659 NNNTDLTPSQAHMALADIDKTEKDALQHIENSNS--IDDINNKEHAFTTLAHI-----4710
Qy 488 INGEVLVDENSRLVTLTKSYLRETLATDLSNKEKLIYPPNGFIS--NIVENGNLEG 545
Db 4711 -----IWDTDQQLVPELPELSQNALVT-----SEVVHREDTISLESIIIGAMTLTD 4759
Qy 546 ENLEPWKAN-----NKAAVUDHTGGVNGTKVLYVHDEGESEOF-----IGDKL 588
Db 4760 E-----LKNIVLSLPRTDKVADHL-----TAKVKVILADSFYTVVNVPVKVEKELOIAKGD 4811
Qy 589 KLTKEVYIYIVKGAATYLDKDEKNQGYIYEETNNLEDPQAVTKR 634
Db 4812 AIKT---IDVLVKOK---IKDIDSNN--ELTSTOREDAPAEIER 4847

RESULT 15
US-11-045-004-34
Sequence 34, Application US/11045004
Publication No. US20060078901A1
GENERAL INFORMATION:
APPLICANT: BUCHRISEER, CARMEN
APPLICANT: FRANGIELU, LIONEL
APPLICANT: COUVE, ELISABETH
APPLICANT: RUSNIOK, CHRISTOPHE
APPLICANT: FSIHI, HAFIDA
APPLICANT: DEHOUX, PIERRE
APPLICANT: DUSURGUT, OLIVIER
APPLICANT: CHETOUANI, FARID
APPLICANT: NEDJARI, HAFED
APPLICANT: GLASER, PHILIPPE
APPLICANT: KUNST, FRANCK
APPLICANT: COSSART, PASCALE
APPLICANT: DANIELS, JUSTIN
APPLICANT: GOEBEL, WERNER
APPLICANT: KREFT, JURGEN
APPLICANT: KIHEN, MICHAEL
APPLICANT: NG, EVA
APPLICANT: VAQUERZ-BOLAND, ANTONIO
APPLICANT: DOMINGUEZ-BERNAL, GUSTAVO
APPLICANT: GARRIDO-GARCIA, PATRICIA
APPLICANT: TIERRERZ-MARTINEZ, ALBERTO
APPLICANT: AMEND, ALEXANDRA
APPLICANT: CHAKRABORTY, TRINAD
APPLICANT: DOMANN, EUGEN
APPLICANT: HAIN, THORSTEN
APPLICANT: BERCHÉ, PATRICK
APPLICANT: CHARBIT, ALAIN
APPLICANT: DURANT, LIONEL
APPLICANT: PEREZ-DIAZ, JOSE-CLAUDIO
APPLICANT: BAQUERO, FERNANDO
APPLICANT: GARCIA DEL PORTILLO, FRANCISCO
APPLICANT: GOMEZ-LOPEZ, NURIA
APPLICANT: MADUENIO, ENCARNIA
APPLICANT: PABLOS, BETRIZ DE
APPLICANT: WEHLAND, JURGEN
APPLICANT: KARST, UWE
APPLICANT: ENTIAN, KARL-DIETER
APPLICANT: HAUF, JOERG
APPLICANT: ROSE, MATTHIAS
APPLICANT: VOSS, HAMUT
TITLE OF INVENTION: LISTERIA MONOCYTOGENES GENOME, POLYPEPTIDES AND USES
FILE REFERENCE: 05394.0018-02
CURRENT APPLICATION NUMBER: US/11/045.004

Qy 10 KALPSPID---YENGIIYGFATG-----IKDINMMI FKNTNGDGLTLDLILKNQOOLNE 59
Db 583 KWDKVIDADQYKNGVFNKYKTEIEMKLI FNDSKLI SKP-----TIEDSLNSGQFFIQ 636
Qy 60 ISGKLDGVNGS---LNDLLAQNLDTREL SKELIKIANEONKVLANDVNTGLDAINIMLNT 115
Db 637 DSIEIHKIDUSANIPQVELLPENYDVTFYTK--ENGNEOVL-----ITFKKPLIHPVEVT 690
Qy 116 YLPKITSMLSDVMKONALGLOIEVLSKQLEISDKLDVINNVVLIINSTLEITPAYORI 175
Db 691 YKTKPVGITRPIYKNAKVIDEGEVADYEAVIDD---NAKRYVKSQEQVDNDIWE 746
Qy 176 KYVNEKEBALTSATEIN-LKT--KODSSHDIIDELTELTELAKSVTKNDVDGEPYLIAT 232
Db 747 IVANQSGSTVSNATVITLTGTQKLDTSIYKYVKSQTSYGMKLOESNMPISPGEDYLT 806
Qy 233 -----PHDWIGNNLGRSALKPASLILAKENIKTSGSISVGNVYNFLIYVTLAQK 283
Db 807 GVDESNLEFYQVFKNEINQSYVYKIQATITLTSDETT-AQIGNSVTF-----855
Qy 284 AFLTLTYCRKLGLADIDYTPIMNENHLNKEKEFRVNI--LPTLSNTPSNPYEKARGS 340
Db 856 -----TGDNITKETEKTNIIEVKITTGDOT-----GT 883
Qy 341 DKDAKIIM---EAKPEYALVFEISKOSIAVLKTYQAKLKNYQ-IDKOSLSB---IYV 392
Db 884 GENTGKIILNKVDRADPSIPLDG-----ATFELYANDEKVDQTQTDKNGVIEFDDLYV 935
Qy 393 GDIDKLLCPQOSQOMYTNKIAFPNEVYTKIAFTKGLNSLRVEYANFDFSSGTDIDLN 452
Db 936 GD-----YTLKEVSAPEGYTL-----TASTENIQV- 961
Qy 453 KKKIESSEAFSMLNANNQGVMPICITSETFLPIINGF-----491
Db 962 --KLEDEQEKVQVMNER-----MPIKETGEVHLVKDKATGATLAGAFELYDKSGAELQ 1014
Qy 492 -GLVDENSRLVTLTKSYLRETLATDLSN---KETKLIYPPNGF- ISN-----IYENG 541
Db 1015 NGLTTENGEL-----TIHNLIDLSYLIKETK--ADEGYLSEKTEWSEFVSIG 1060
Qy 542 NLGEMNLEPKANKN-----AYVDH--TGVNGTKVLYVHDEGESEQ--FIDGKYLAK 591
Db 1061 QVDA--TEIOAEKEDJGAEVLTTRKVSSETNAKLSGAKFNILNDSGEVITQNLVSDR---1114
Qy 592 TEYIYIYVKGKAAIYLDKDEKNQGYIYEETNNLEL-DPQAVTKRF--ITGDSRVHLIF 648
Db 1115 -----NBEIVQNIPEBDYAFQETLEARTYDIAINTMPFTIVAGOTSA---TWV 1160
Qy 649 TSQNGEAFGCFNFTISEIRPSEELSPELIKSDAMVG-----SQGTWISGNLS 696
Db 1161 TAEENKVG-----KPDVDTGEVILIVKQDSATGETLEGAVFLMTADGAIVAS---1207

Query Match 4.0%; Score 159; DB 11; Length 1530;
Best Local Similarity 19.3%; Pred. No. 0.46;
Matches 166; Conservative 122; Mismatches 294; Indels 276; Gaps 43;

```
Oy 697 NINNVNCTFR-QNISLESYS-----TYSNPNVNGFGKVTIRNSREVVFERSYLOF 747
    | : : | | | : : | | | : : |
Db 1208 NLTTDANGELIYVNLAPGKYSFKETKAPEGEYELATDVWEF---TIAPNQ----- 1253
Oy 748 SSKYISEKFTTTNNYGL 765
    | | | | | | | |
Db 1254 -----PEKITTTAENTKL 1266
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Search completed: May 15, 2006, 20:48:27
Job time : 34 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 15, 2006, 20:48:06 / Search time 188 Seconds
(without alignments)
1836.977 Million cell updates/sec

Title: US-10-698-096-17

Perfect score: 786
Sequence: 1 MQNNKLGVXALPSPFIDYFN.....VELSRASSRGVINGDFSIK 786

Scoring table: **OMIGO**
Gapop 60.0, Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word size 8

Total number of hits satisfying chosen parameters: 2442881

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

A_Geneseq_21.*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	5.9	787	7 ADD43701	Add43701 Bacillus
2	45	5.7	787	3 AAY59284	Aay59284 SDP toxin
3	45	5.7	787	8 ADG88542	Adg88542 Bacillus
4	43	5.5	511	2 AAW46865	Aaw46865 Bacillus
5	43	5.5	511	2 AAY24968	Aay24968 Bacillus
6	43	5.5	759	2 AAW46864	Aaw46864 Bacillus
7	43	5.5	759	2 AAY24967	Aay24967 Bacillus
8	43	5.5	786	7 ADD43705	Add43705 Bacillus
9	43	5.5	787	6 ABB82567	Abb82567 B. thurin
10	43	5.5	787	6 ABB82565	Abb82565 B. thurin
11	43	5.5	787	6 ABB82565	Abb82565 B. thurin
12	43	5.5	787	7 ADN08758	Adn08758 B. thurin
13	43	5.5	788	7 ADD43703	Add43703 Bacillus
14	43	5.5	788	7 ADN08783	Adn08783 B. thurin
15	43	5.5	789	2 AAW60216	Aaw60216 Bacillus
16	43	5.5	789	2 AAW60217	Aaw60217 Bacillus
17	43	5.5	789	2 AAW46862	Aaw46862 Bacillus
18	43	5.5	789	2 AAW46863	Aaw46863 Bacillus
19	43	5.5	789	2 AAW46868	Aaw46868 Bacillus
20	43	5.5	789	2 AAW46867	Aaw46867 Bacillus
21	43	5.5	789	2 AAW46869	Aaw46869 Bacillus
22	43	5.5	789	2 AAW46866	Aaw46866 Bacillus
23	43	5.5	789	2 AAW46861	Aaw46861 Bacillus
24	43	5.5	789	2 AAY24971	Aay24971 Bacillus

25	43	5.5	789	2 AAY24966	Aay24966 Bacillus
26	43	5.5	789	2 AAY24970	Aay24970 Bacillus
27	43	5.5	789	2 AAY24974	Aay24974 Bacillus
28	43	5.5	789	2 AAY24972	Aay24972 Bacillus
29	43	5.5	789	2 AAY24965	Aay24965 Bacillus
30	43	5.5	789	2 AAY24964	Aay24964 Bacillus
31	43	5.5	789	2 AAY24969	Aay24969 Bacillus
32	43	5.5	789	6 ABB82566	Abb82566 B. thurin
33	43	5.5	789	7 ADN08756	Adn08756 B. thurin
34	43	5.5	790	2 AAW60215	Aaw60215 Bacillus
35	43	5.5	790	2 AAW46872	Aaw46872 Bacillus
36	43	5.5	790	2 AAW46871	Aaw46871 Bacillus
37	43	5.5	790	2 AAY24975	Aay24975 Bacillus
38	43	5.5	790	3 AAY59275	Aay59275 Toxin fro
39	43	5.5	790	8 ADG88492	Adg88492 Bacillus
40	41	5.2	789	2 AAW46860	Aaw46860 Bacillus
41	41	5.2	789	2 AAY24963	Aay24963 Bacillus
42	38	4.8	789	7 ADN08753	Adn08753 B. thurin
43	35	4.5	789	2 AAR91243	Aar91243 B. thurin
44	35	4.5	789	2 AAW19514	Aaw19514 B. cereus
45	35	4.5	789	2 AAW46725	Aaw46725 Vegetativ

ALIGNMENTS

RESULT 1
ADD43701
ID ADD43701 standard; protein; 787 AA.
AC ADD43701;
XX
DT 15-JAN-2004 (first entry)
XX
DE Bacillus thuringiensis insecticidal protein ISP3-1099E.
XX
KM Insecticidal; plant insect pest; pesticide.
XX
OS Bacillus thuringiensis.
XX
PN WO2003080656-A1.
XX
PD 02-OCT-2003.
XX
PF 20-MAR-2003; 2003WO-EP003068.
XX
PR 22-MAR-2002; 2002US-0366276P.
XX
PR 06-NOV-2002; 2002US-0423999P.
XX
PA (PARB) BAYER BIOSCIENCE NV.
XX
PI Arnaut G, Boets A, De Rudder K, Vanneste S, Van Rie J;
XX
DR WPI; 2003-876903/81.
XX
DR N-PSDB; ADD43700.
XX
PT New insecticidal proteins, useful for controlling plant insect pests, and
PT for increasing resistance to insect damage compared to control plants.
XX
PS Claim 3; SEQ ID NO 2; 81bp; English.
XX
CC The present invention relates to Bacillus thuringiensis insecticidal
CC proteins (ADD43701, ADD43703 and ADD43705) and their coding sequences
CC (ADD43700, ADD43702 and ADD43704). The insecticidal proteins are
CC insecticidal against Helicoverpa zea, Heliothis virescens, Ostrinia
CC nubilalis, Spodoptera frugiperda, Agrotis ipsilon, Pectinophora
CC gossypiella, Scirphophaga incertulan, Graphollocoris medinalis, Sesamia
CC inferens, Chilo partellus and Anticarsia gemmatilis. The proteins are
CC useful for controlling plant insect pests, and for increasing resistance
CC to insect damage compared to control plants.
XX
SQ Sequence 787 AA;

Query Match 5.9%; Score 46; DB 7; Length 787;
 Best Local Similarity 100.0%; Pred. No. 3.9e-39;
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 514 LLATDSNKEFKIIVPENGFSINIVENGNGENLBPWKANNKNAY 559
 DB 515 LLATDSNKEFKIIVPENGFSINIVENGNGENLBPWKANNKNAY 560

RESULT 2
 ID AAY59284
 AC AAY59284;
 DT 18-APR-2000 (first entry)

XX SUP toxin from B. thuringiensis strain KB59A4-6.
 XX

KW Bacillus thuringiensis; toxin; endotoxin; pesticide; plant pest;
 KM Lepidoptera; cleopteraans.

OS Bacillus thuringiensis.

PN WO957282-A2.

PD 11-NOV-1999.

PF 06-MAY-1999; 99WO-US009997.

PR 06-MAY-1998; 98US-00073898.

XX (MYCO) MYCOGEN CORP.

PI Feltelson JS, Schepf HE, Narva KE, Stockhoff BA, Schmeits J;
 PI Loewer D, Dullum CJ, Muller-Cohn J, Stamp L, Morrill G;

PI Finstad-Lee S;

DR WPI; 2000-096811/08.

DR N-PSDB; AA258823.

PT New polynucleotides encoding pesticidally active proteins, useful for
 PT transforming plants for controlling pests.

PS Claim 2; Page 100-103; 104pp; English.

XX The invention relates to novel B. thuringiensis isolates, and genes
 CC encoding pesticidal toxins which are toxic to non-mammalian pests. The
 CC genes are useful in the control of non-mammalian pests and especially
 CC plant pests (e.g. lepidopteraans and/or cleopteraans). The polynucleotides
 CC are useful for transforming plants for controlling plant pests; for
 CC designing primers and probes useful for the identification and
 CC characterization of genes which encode pesticidal toxins. The present
 CC sequence represents a B.t. SUP toxin

XX Sequence 787 AA;

Query Match 5.7%; Score 45; DB 3; Length 787;
 Best Local Similarity 100.0%; Pred. No. 4.6e-38;
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 139 EYLSKQLKEISDKLDVINNVNLINSTLTETTPAYORIKYNEKFE 183
 DB 140 EYLSKQLKEISDKLDVINNVNLINSTLTETTPAYORIKYNEKFE 184

RESULT 3
 ID ADG88542
 AC ADG88542;
 DT 11-MAR-2004 (first entry)

XX Bacillus thuringiensis strain KB59A4-6 SUP toxin protein.
 DE Pesticide; genetic engineering; resistance; toxin; insecticide;
 XX plant protectant; gene; ds.

OS Bacillus thuringiensis.

PN US603063-B1.

PD 05-AUG-2003.

PF 07-MAY-1999; 99US-00307106.

PR 07-MAY-1999; 99US-00307106.

XX (MYCO) MYCOGEN CORP.

PI Feltelson JS, Schepf HE, Narva KE, Stockhoff BA, Schmeits J;
 PI Loewer D, Dullum CJ, Muller-Cohn J, Stamp L, Morrill G;

PI Finstad-Lee S;

DR WPI; 2004-008371/01.

DR N-PSDB; ADG88541.

PT New polynucleotide from Bacillus subtilis, which encodes delta endotoxins
 PT or pesticide proteins, useful in plant genetic engineering, particularly
 PT for producing plants that are resistant to lepidopteran or coleopteran
 PT pests.

PS Claim 1; SEQ ID NO 54; 51pp; English.

XX The present invention provides an isolated polynucleotide from Bacillus
 CC thuringiensis (B.t.) strain KB59A4-6 that encodes an active pesticidal
 CC SUP toxin protein. The invention is useful in plant genetic engineering
 CC particularly producing plants that express such gene in order to
 CC effectively control various insects e.g. boll weevil, black cutworm etc.
 CC The invention is also useful for conferring resistance in plants against
 CC lepidopteraans or coleopteraans. The present sequence is Bacillus
 CC thuringiensis protein.

XX Sequence 787 AA;

Query Match 5.7%; Score 45; DB 8; Length 787;
 Best Local Similarity 100.0%; Pred. No. 4.6e-38;
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 139 EYLSKQLKEISDKLDVINNVNLINSTLTETTPAYORIKYNEKFE 183
 DB 140 EYLSKQLKEISDKLDVINNVNLINSTLTETTPAYORIKYNEKFE 184

RESULT 4
 ID AAW46865
 AC AAW46865;
 DT 11-JUN-1998 (first entry)

XX Bacillus thuringiensis toxin designated 94R1(a).
 DE

KW Toxin; lepidopteran pest; control; Agrotis ipsilon; black cutworm;
 KM Heliothis virescens; Helicoverpa zea.

OS Bacillus thuringiensis.

PN WO9800546-A2.

PD 08-JAN-1998.

PF 01-JUL-1997; 97WO-US011658.

PR 01-JUL-1996; 96US-00674002.
XX
XX (MYCOG) MYCOGEN CORP.
XX
PI Schnepf HE, Wicker C, Narva KE, Walz M, Stockhoff BA;
XX
DR WPI; 1998-086971/08.
XX
DR N-PSDB; AAV16524.
XX
XX New isolated *Bacillus thuringiensis* isolate(s) - used to obtain genes
PT encoding toxins which are active against lepidopteran pests such as the
PT Black cutworm.
XX
PS Claim 42; Page 131-133; 183pp; English.
XX
XX The present sequence represents a *Bacillus thuringiensis* toxin which is
CC active against lepidopteran pests. The toxin isolates can be used for the
CC control of lepidopteran pests such as *Agrotis ipsilon* (black cutworm),
CC *Heliothis virescens* and *Helicoverpa zea*. PCR primers and probes can be
CC derived from the polynucleotide encoding the toxin and used for the
CC amplification and detection of other toxin-encoding sequences
XX
SO Sequence 511 AA;

Query Match 5.5%; Score 43; DB 2; Length 511;
Best Local Similarity 100.0%; Pred. No. 4.2e-36;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 KTSSEVGNVNFILVLTALQAKAFLTTTCRKLGLADIDYT 303
DB 122 KTSSEVGNVNFILVLTALQAKAFLTTTCRKLGLADIDYT 164

RESULT 5
AA124968
ID AAV24968 standard; protein; 511 AA.
XX
AC AAV24968;
XX
DT 09-SEP-1999 (first entry)
XX
DE *Bacillus thuringiensis* toxin 94R1(a).
XX
XX *Bacillus thuringiensis*; toxin; *Ostrinia nubilalis*; lepidopteran;
KM European corn borer; black cutworm.
XX
OS *Bacillus thuringiensis*.
XX
PN WO9933991-A2.
XX
PD 08-JUL-1999.
XX
PF 15-DEC-1998; 98WO-US026585.
XX
PR 31-DEC-1997; 97US-00002285.
XX
PA (MYCOG) MYCOGEN CORP.
XX
PI Schnepf HE, Wicker C, Narva KE, Walz M, Stockhoff BA;
PI Muller-Cohn J;
XX
XX WPI; 1999-405513/34.
DR N-PSDB; AAX83885.
XX
XX Method for control of European corn borer using *Bacillus thuringiensis*
PT toxins.
XX
PS Claim 1; Page 135-137; 174pp; English.
XX
XX A method has been developed for the control of European corn borer
CC (*Ostrinia nubilalis*), comprising contacting the pest with a pesticidal
CC amount of a *Bacillus thuringiensis* toxin. The method is used for the
CC control of European corn borer (*Ostrinia nubilalis*). The method can also

CC be used for the control of other non-mammalian pests, particularly black
CC cutworm, and other lepidopteran pests. The present sequence represents a
CC *Bacillus thuringiensis* toxin from the present invention
XX
SO Sequence 511 AA;

Query Match 5.5%; Score 43; DB 2; Length 511;
Best Local Similarity 100.0%; Pred. No. 4.2e-36;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 KTSSEVGNVNFILVLTALQAKAFLTTTCRKLGLADIDYT 303
DB 122 KTSSEVGNVNFILVLTALQAKAFLTTTCRKLGLADIDYT 164

RESULT 6
AAW46864
ID AAW46864 standard; protein; 759 AA.
XX
AC AAW46864;
XX
DT 11-JUN-1998 (first entry)
XX
XX *Bacillus thuringiensis* toxin designated 86W1(a).
DE
XX Toxin; lepidopteran pest; control; *Agrotis ipsilon*; black cutworm;
KM *Heliothis virescens*; *Helicoverpa zea*.
XX
XX *Bacillus thuringiensis*.
OS
XX
FH Key Location/Qualifiers
FT Misc-difference 193
FT /label= unknown
FT /note= "encoded by AKT"
FT /label= unknown
FT /note= "encoded by AST"
XX
PN WO9800546-A2.
XX
XX 08-JAN-1998.
PD
XX
PF 01-JUL-1997; 97WO-US011658.
XX
PR 01-JUL-1996; 96US-00674002.
XX
XX (MYCOG) MYCOGEN CORP.
XX
PI Schnepf HE, Wicker C, Narva KE, Walz M, Stockhoff BA;
XX
XX WPI; 1998-086971/08.
DR N-PSDB; AAV16523.
XX
XX New isolated *Bacillus thuringiensis* isolate(s) - used to obtain genes
PT encoding toxins which are active against lepidopteran pests such as the
PT Black cutworm.
XX
PS Claim 42; Page 126-129; 183pp; English.
XX
XX The present sequence represents a *Bacillus thuringiensis* toxin which is
CC active against lepidopteran pests. The toxin isolates can be used for the
CC control of lepidopteran pests such as *Agrotis ipsilon* (black cutworm),
CC *Heliothis virescens* and *Helicoverpa zea*. PCR primers and probes can be
CC derived from the polynucleotide encoding the toxin and used for the
CC amplification and detection of other toxin-encoding sequences. note:
CC nucleotide sequence contains numerous stop codons which do not alter the
CC reading frame
XX
SO Sequence 759 AA;

Query Match 5.5%; Score 43; DB 2; Length 759;
Best Local Similarity 100.0%; Pred. No. 6.1e-36;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      261 KTSGSEGVNPNFLIVLTALQAKAFLLTTCRKLGLADIDYT 303
      |||
      262 KTSGSEGVNPNFLIVLTALQAKAFLLTTCRKLGLADIDYT 304

Db

RESULT 7
AAY24967
ID      AAY24967 standard; protein; 759 AA.
XX
XX
AC      AAY24967;
XX
XX
DT      09-SEP-1999 (first entry)
XX
XX
DE      Bacillus thuringiensis toxin 86W1(a).
XX
XX
KM      Bacillus thuringiensis; toxin; Ostrinia nubilalis; lepidopteran;
XX
XX
KM      European corn borer; black cutworm.
XX
XX
OS      Bacillus thuringiensis.
XX
XX
FH      Key Location/Qualifiers
FT      Misc-difference 193 /note= "unspecified"
FT      Misc-difference 257 /note= "unspecified"
XX
XX
PN      WO9933991-A2.
XX
XX
PD      08-JUL-1999.
XX
XX
PF      15-DEC-1998; 98WO-US026585.
XX
XX
PR      31-DEC-1997; 97US-00002285.
XX
XX
PA      (MYCO ) MYCOGEN CORP.
XX
XX
PI      Schaepe HE, Wicker C, Narva KE, Walz M, Stockhoff BA;
XX
XX
PI      Muller-Cohn J;
XX
XX
DR      WPI: 1999-405513/34.
XX
XX
DR      N-PSDB; AAX83884.
XX
XX
PT      Method for control of European corn borer using Bacillus thuringiensis
XX
XX
PT      toxins.
XX
XX
PS      Claim 1; Page 130-133; 174pp; English.
XX
XX
CC      A method has been developed for the control of European corn borer
XX
XX
CC      (Ostrinia nubilalis), comprising contacting the pest with a pesticidal
XX
XX
CC      amount of a Bacillus thuringiensis toxin. The method is used for the
XX
XX
CC      control of European corn borer (Ostrinia nubilalis). The method can also
XX
XX
CC      be used for the control of other non-mammalian pests, particularly black
XX
XX
CC      cutworm, and other lepidopteran pests. The present sequence represents a
XX
XX
CC      Bacillus thuringiensis toxin from the present invention
XX
XX
SQ      Sequence 759 AA;

Query Match      5.5%; Score 43; DB 2; Length 759;
Best Local Similarity 100.0%; Pred. No. 6.1e-36;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      261 KTSGSEGVNPNFLIVLTALQAKAFLLTTCRKLGLADIDYT 303
      |||
      262 KTSGSEGVNPNFLIVLTALQAKAFLLTTCRKLGLADIDYT 304

Db

RESULT 8
ADD43705
ID      ADD43705 standard; protein; 786 AA.
XX
XX
AC      ADD43705;
XX
XX

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```

DT      15-JAN-2004 (first entry)
XX
XX
DE      Bacillus thuringiensis insecticidal protein ISPJ-2245J.
XX
XX
KM      Insecticidal; plant insect pest; pesticide.
XX
XX
XX      Bacillus thuringiensis.
XX
XX
XX      WO2003080656-A1.
XX
XX
PD      02-OCT-2003.
XX
XX
PF      20-MAR-2003; 2003WO-EP003068.
XX
XX
PR      22-MAR-2002; 2002US-0366276P.
XX
XX
PR      06-NOV-2002; 2002US-0423999P.
XX
XX
PA      (FARB ) BAYER BIOSCIENCE NV.
XX
XX
PI      Arnaud G, Boets A, De Rudder K, Vanneste S, Van Rie J;
XX
XX
XX      WPI; 2003-876903/81.
XX
XX
DR      N-PSDB; ADD43704.
XX
XX
PT      New insecticidal proteins, useful for controlling plant insect pests, and
XX
XX
PT      for increasing resistance to insect damage compared to control plants.
XX
XX
PS      Claim 2; SEQ ID NO 6; 81pp; English.
XX
XX
XX      The present invention relates to Bacillus thuringiensis insecticidal
XX
XX
CC      proteins (ADD43701, ADD43703 and ADD43705) and their coding sequences
XX
XX
CC      (ADD43700, ADD43702 and ADD43704). The insecticidal proteins are
XX
XX
CC      insecticidal against Helicoverpa zea, Helicoverpa virescens, Ostrinia
XX
XX
CC      nubilalis, Spodoptera frugiperda, Agrotis ipsilon, Pectinophora
XX
XX
CC      gossypiella, Scirphophaga incertulans, Chaptalia medialis, Sesamia
XX
XX
CC      inferens, Chilo partellus and Anticarsia gemmatilis. The proteins are
XX
XX
CC      useful for controlling plant insect pests, and for increasing resistance
XX
XX
CC      to insect damage compared to control plants.
XX
XX
SQ      Sequence 786 AA;

Query Match      5.5%; Score 43; DB 7; Length 786;
Best Local Similarity 100.0%; Pred. No. 6.3e-36;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      261 KTSGSEGVNPNFLIVLTALQAKAFLLTTCRKLGLADIDYT 303
      |||
      262 KTSGSEGVNPNFLIVLTALQAKAFLLTTCRKLGLADIDYT 304

Db

RESULT 9
ABB82567
ID      ABB82567 standard; protein; 787 AA.
XX
XX
AC      ABB82567;
XX
XX
XX      04-FEB-2003 (first entry)
XX
XX
DT      04-FEB-2003 (first entry)
XX
XX
DE      B. thuringiensis hybrid Vip3A-B toxin.
XX
XX
XX      Vip3; toxin; insecticide; transgenic; delta-endotoxin; Vip3B; Vip3A.
XX
XX
XX      Bacillus thuringiensis.
XX
XX
XX      WO200278437-A2.
XX
XX
XX      10-OCT-2002.
XX
XX
XX      01-APR-2002; 2002WO-US010264.
XX
XX
XX      30-MAR-2001; 2001US-0280025P.
XX
XX
XX      04-DEC-2001; 2001US-033657P.
XX
XX

```

PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
PI Miles P, Kramer V, Shen Z, Shockoski F, Warren GW;
XX WPI: 2003-040603/03.
DR N-PSDB; ABV74980.
XX
PT Novel pesticidal toxin, designated Vip3 toxins from *Bacillus*
thuringiensis, useful for controlling insects, e.g., lepidopteran insect,
is highly active against a wide range of insect pests.
XX
PS Example 9; Page 73-76; 82pp; English.
XX
CC The invention relates to an isolated Vip3 toxin from *B. thuringiensis*
CC that is active against insects. The toxins are useful for controlling
CC insects, where the insect is a lepidopteran insect selected from *Ostrinia*
CC *nubilalis* (European corn borer), *Plutella xylostella* (diamondback moth),
CC *Spodoptera frugiperda* (fall armyworm), *Agrotis ipsilon* (black cutworm),
CC *Helicoverpa zea* (corn earworm), *Heliothis virescens* (tobacco budworm), *S.*
CC *exigua* (beet armyworm), *Helicoverpa punctigera* (native budworm), *S.*
CC *Trichoplusia ni* (cabbage looper), *Pectinophora gossypiella* (pink
CC bollworm), and *Cochylis hospes* (banded sunflower moth). The
CC polynucleotides encoding the toxins are useful to produce an insect-
CC resistant transgenic plant. The toxins are useful in combination with Bt
CC delta-endotoxins to increase pest target range. The present sequence
CC represents a *B. thuringiensis* Vip3A-B hybrid toxin
XX
SQ Sequence 787 AA;
XX
Query Match 5.5%; Score 43; DB 6; Length 787;
Best Local Similarity 100.0%; Pred. No. 6.3e-36;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 261 KTSGSEVGNVNNFLIVLTALQAKAFLLTTCRKILGLADIDYT 303
DB 262 KTSGSEVGNVNNFLIVLTALQAKAFLLTTCRKILGLADIDYT 304
XX
RESULT 10
ABB82565
ID ABB82565 standard; protein: 787 AA.
XX
AC ABB82565;
XX
DT 04-FEB-2003 (first entry)
XX
DE *B. thuringiensis* native Vip3B polypeptide.
XX
KM Vip3; toxin; insecticide; transgenic; delta-endotoxin; Vip3B.
XX
OS *Bacillus thuringiensis*.
XX
PN WO200278437-A2.
XX
PD 10-OCT-2002.
XX
PF 01-APR-2002; 2002WO-US010264.
XX
PR 30-MAR-2001; 2001US-0280025P.
PR 04-DEC-2001; 2001US-0336657P.
XX
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
PI Miles P, Kramer V, Shen Z, Shockoski F, Warren GW;
XX
DR WPI: 2003-040603/03.
DR N-PSDB; ABV74977.
XX
PT Novel pesticidal toxin, designated Vip3 toxins from *Bacillus*
thuringiensis, useful for controlling insects, e.g., lepidopteran insect,
is highly active against a wide range of insect pests.
XX

PS Claim 4; Page 56-60; 82pp; English.
XX
CC The invention relates to an isolated Vip3 toxin from *B. thuringiensis*
CC that is active against insects. The toxins are useful for controlling
CC insects, where the insect is a lepidopteran insect selected from *Ostrinia*
CC *nubilalis* (European corn borer), *Plutella xylostella* (diamondback moth),
CC *Spodoptera frugiperda* (fall armyworm), *Agrotis ipsilon* (black cutworm),
CC *Helicoverpa zea* (corn earworm), *Heliothis virescens* (tobacco budworm), *S.*
CC *exigua* (beet armyworm), *Helicoverpa punctigera* (native budworm), *S.*
CC *Trichoplusia ni* (cabbage looper), *Pectinophora gossypiella* (pink
CC bollworm), and *Cochylis hospes* (banded sunflower moth). The
CC polynucleotides encoding the toxins are useful to produce an insect-
CC resistant transgenic plant. The toxins are useful in combination with Bt
CC delta-endotoxins to increase pest target range. The present sequence
CC represents a *B. thuringiensis* Vip3B toxin
XX
SQ Sequence 787 AA;
XX
Query Match 5.5%; Score 43; DB 6; Length 787;
Best Local Similarity 100.0%; Pred. No. 6.3e-36;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 261 KTSGSEVGNVNNFLIVLTALQAKAFLLTTCRKILGLADIDYT 303
DB 262 KTSGSEVGNVNNFLIVLTALQAKAFLLTTCRKILGLADIDYT 304
XX
RESULT 11
ADN08758
ID ADN08758 standard; protein: 787 AA.
XX
AC ADN08758;
XX
DT 17-JUN-2004 (first entry)
XX
DE *B. thuringiensis* Vip3B protein SEQ ID NO:7.
XX
KM Vip3C; toxin; protease inhibitor; lepidopteron; tobacco budworm;
KM sunflower head moth; beet armyworm; insect-resistance; maize; Vip3B.
XX
OS *Bacillus thuringiensis*.
XX
PN WO2003075655-A2.
XX
PD 18-SEP-2003.
XX
PF 20-FEB-2003; 2003WO-US004735.
XX
PR 06-MAR-2002; 2002US-0362250P.
XX
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
PI Shen Z, Warren GW, Shockoski F, Kramer V;
XX
DR WPI: 2003-788166/74.
DR N-PSDB; ADN08757.
XX
PT New Vip3 toxin encoded by a nucleic acid from *Bacillus thuringiensis*,
PT useful for controlling lepidopteran insects such as tobacco budworm,
PT sunflower head moth or beet armyworm, or for producing an insect-
PT resistant transgenic plant.
XX
PS Example 10; SEQ ID NO 7; 11pp; English.
XX
CC The invention relates to a novel isolated Vip3 toxin that is active
CC against insects. The toxin acts as a protease inhibitor. The Vip3 toxin,
CC hybrid toxin and nucleic acid molecules are useful for controlling
CC lepidopteron insects such as tobacco budworm, sunflower head moth or beet
CC armyworm, for producing an insect-resistant transgenic plant, and
CC protecting a maize plant against at least one insect pest. The present
CC sequence represents native *B. thuringiensis* Vip3B.
XX

SQ Sequence 787 AA;

Query Match 5.5%; Score 43; DB 7; Length 787;

Best Local Similarity 100.0%; Pred. No. 6.3e-36; Mismatches 0; Indels 0; Gaps 0;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 KTSGSEVGVNVLIVLTALQAKAFLLTTCRKLGLADIDYT 303
 |||||
 DB 262 KTSGSEVGVNVLIVLTALQAKAFLLTTCRKLGLADIDYT 304

RESULT 12

ADD43703
 ID ADD43703 standard; protein; 788 AA.

AC ADD43703;

DT 15-JUN-2004 (first entry)

DE *Bacillus thuringiensis* insecticidal protein ISP3-327D.

XX Insecticidal; plant insect pest; pesticide.

XX *Bacillus thuringiensis*.

XX WO2003080656-A1.

XX 02-OCT-2003.

XX 20-MAR-2003; 2003WO-EP003068.

XX 22-MAR-2002; 2002US-0366276P.

XX 06-NOV-2002; 2002US-0423999P.

XX (FARB) BAYER BIOSCIENCE NV.

XX Arnaud G, Boets A, De Rudder K, Vanneste S, Van Rie J;

XX WPI; 2003-876903/81.

XX N-PSDB; ADD43702.

XX New insecticidal proteins, useful for controlling plant insect pests, and

XX for increasing resistance to insect damage compared to control plants.

XX Claim 1; SEQ ID NO 4; 81bp; English.

XX The present invention relates to *Bacillus thuringiensis* insecticidal
 CC proteins (ADD43701, ADD43703 and ADD43705) and their coding sequences
 CC (ADD43700, ADD43702 and ADD43704). The insecticidal proteins are
 CC insecticidal against *Helicoverpa zea*, *Heliothis virescens*, *Ostrinia*
 CC *nubilalis*, *Spodoptera frugiperda*, *Agrotis ipsilon*, *Pectinophora*
 CC *gossypiella*, *Scirphophaga incertulans*, *Gnathocroci medialis*, *Sesamia*
 CC *inferens*, *Chilo partellus* and *Anticarsia gemmatilis*. The proteins are
 CC useful for controlling plant insect pests, and for increasing resistance
 CC to insect damage compared to control plants.

SQ Sequence 788 AA;

Query Match 5.5%; Score 43; DB 7; Length 788;

Best Local Similarity 100.0%; Pred. No. 6.3e-36; Mismatches 0; Indels 0; Gaps 0;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 KTSGSEVGVNVLIVLTALQAKAFLLTTCRKLGLADIDYT 303
 |||||
 DB 262 KTSGSEVGVNVLIVLTALQAKAFLLTTCRKLGLADIDYT 304

RESULT 13

ADN08783
 ID ADN08783 standard; protein; 788 AA.

XX ADN08783;

XX

DT 17-JUN-2004 (first entry)

DE *B. thuringiensis* vip3C-12168 protein SEQ ID NO:32.XX *vip3c*; toxin; protease inhibitor; lepidopteron; tobacco budworm;

XX sunflower head moth; beet armyworm; insect-resistance; maize.

XX *Bacillus thuringiensis*.

XX WO2003075655-A2.

XX 18-SEP-2003.

XX 20-FEB-2003; 2003WO-US004735.

XX 06-MAR-2002; 2002US-0362250P.

XX (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Shen Z, Warren GW, Shokoski F, Kramer V;

XX WPI; 2003-788166/74.

XX N-PSDB; ADN08782.

XX New *Vip3* toxin encoded by a nucleic acid from *Bacillus thuringiensis*,

XX useful for controlling lepidopteran insects such as tobacco budworm,

XX sunflower head moth or beet armyworm, or for producing an insect-

XX resistant transgenic plant.

XX Claim 12; SEQ ID NO 32; 118bp; English.

XX The invention relates to a novel isolated *Vip3* toxin that is activeXX against insects. The toxin acts as a protease inhibitor. The *Vip3* toxin,

XX hybrid toxin and nucleic acid molecules are useful for controlling

XX lepidopteron insects such as tobacco budworm, sunflower head moth or beet

XX armyworm, for producing an insect-resistant transgenic plant, and

XX CC protecting a maize plant against at least one insect pest. The present

XX sequence represents *Vip3C* protein *Vip3C*-12168.

XX SQ Sequence 788 AA;

Query Match 5.5%; Score 43; DB 7; Length 788;

Best Local Similarity 100.0%; Pred. No. 6.3e-36; Mismatches 0; Indels 0; Gaps 0;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 KTSGSEVGVNVLIVLTALQAKAFLLTTCRKLGLADIDYT 303
 |||||
 DB 262 KTSGSEVGVNVLIVLTALQAKAFLLTTCRKLGLADIDYT 304

RESULT 14
 ADN08762
 ID ADN08762 standard; protein; 788 AA.

XX ADN08762;

XX 17-JUN-2004 (first entry)

XX *B. thuringiensis* vip3A-C fusion protein SEQ ID NO:11.XX *vip3c*; toxin; protease inhibitor; lepidopteron; tobacco budworm;XX sunflower head moth; beet armyworm; insect-resistance; maize; *Vip3A-C*.XX *Bacillus thuringiensis*.

XX Chimeric.

XX WO2003075655-A2.

XX 18-SEP-2003.

XX 20-FEB-2003; 2003WO-US004735.

XX 06-MAR-2002; 2002US-0362250P.

```

XX (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
XX PI Shen Z, Warren GW, Shokoski F, Kramer V;
XX WPI; 2003-788166/74.
XX DR N-PSDB; ADN08761.
XX
XX PT New Vip3 toxin encoded by a nucleic acid from Bacillus thuringiensis,
XX PT useful for controlling lepidopteran insects such as tobacco budworm,
XX PT sunflower head moth or beet armyworm, or for producing an insect-
XX PT resistant transgenic plant.
XX
XX SQ Claim 12; SEQ ID NO 11; 118bp; English.
XX
XX CC The invention relates to a novel isolated Vip3 toxin that is active
XX CC against insects. The toxin acts as a protease inhibitor. The Vip3 toxin,
XX CC hybrid toxin and nucleic acid molecules are useful for controlling
XX CC lepidopteran insects such as tobacco budworm, sunflower head moth or beet
XX CC armyworm, for producing an insect-resistant transgenic plant, and
XX CC protecting a maize plant against at least one insect pest. The present
XX CC sequence represents vip3-C, a B. thuringiensis vip3A-vip3C fusion
XX CC protein.
XX
XX SQ Sequence 788 AA;
XX
XX Query Match          5.5%; Score 43; DB 7; Length 788;
XX Best Local Similarity 100.0%; Pred. No. 6.3e-36;
XX Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 261 KTSGEVGNVYNNFLIVLTALQAKAFLTTTCRKLLGLADIDYT 303
XX      |||||
XX Db 262 KTSGEVGNVYNNFLIVLTALQAKAFLTTTCRKLLGLADIDYT 304
XX
XX RESULT 15
XX AAW60216
XX ID AAW60216 standard; protein; 789 AA.
XX
XX AC AAW60216;
XX
XX DT 17-OCT-2003 (revised)
XX DT 28-SEP-1998 (first entry)
XX
XX DE Bacillus thuringiensis insecticidal 81F toxin.
XX
XX KW Insecticide; pesticide; toxin; biological control; lepidopteran;
XX KW coleopteran.
XX
XX OS Bacillus thuringiensis; strain PS81F (NRRL B-18424).
XX
XX PN MO9818932-A2.
XX
XX PD 07-MAY-1998.
XX
XX PF 30-OCT-1997; 97MO-US019804.
XX
XX PR 30-OCT-1996; 96US-0029848P.
XX
XX (MYCO ) MYCOGEN CORP.
XX
XX PI Feltelson JS, Schnepf HR, Narva KE, Stockhoff BA, Schmeits JL,
XX PI Loewer D, Schwab G, Dullum CJ, Muller-cohn J, Stamp L;
XX DR WPI; 1998-272226/24.
XX DR N-PSDB; AAV30289.
XX
XX PT Bacillus thuringiensis isolates - used for producing pesticidal toxins
XX PT and nucleotide sequences for control of lepidopterans and coleopterans.
XX
XX PS Example 4; Page 51-53; 139pp; English.
XX
XX This polypeptide comprises the novel 81F toxin of isolate PS81F of

```

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CC Bacillus thuringiensis (B.t.). Its amino acid sequence was deduced from
CC DNA (see AAV30289) isolated by PCR amplification following
CC identification of PS81F as a producer of lepidopteran- active toxin.
CC Disclosed and claimed are novel B.t. isolates, pesticidal toxins (see
CC AAW60215-32), genes and nucleotide probes and primers (see AAV30288-321
CC and AAV99734-87) for the identification of genes encoding toxins active
CC against pests, and transformed host cells. The invention provides
CC entirely new families of toxins from Bacillus isolates. (Updated on 17-
CC OCT-2003 to standardise OS field)
XX
XX SQ Sequence 789 AA;
XX
XX Query Match          5.5%; Score 43; DB 2; Length 789;
XX Best Local Similarity 100.0%; Pred. No. 6.3e-36;
XX Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 261 KTSGEVGNVYNNFLIVLTALQAKAFLTTTCRKLLGLADIDYT 303
XX      |||||
XX Db 262 KTSGEVGNVYNNFLIVLTALQAKAFLTTTCRKLLGLADIDYT 304
XX
XX Search completed: May 15, 2006, 20:51:37
XX Job time : 189 secs

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GenCore version 5.1.8
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OM protein - protein search, using SW model

Run on: May 15, 2006, 20:51:56 ; Search time 44 Seconds
(without alignments)
1718.781 Million cell updates/sec

Title: US-10-698-096-17

Perfect score: 786

Sequence: 1 MQKNKLKSVKALPSFIDYFN.....VELSRASRGVINFDFSIR 786

Scoring table: OLIGO

Gapop 60.0 , Gapept 60.0

Searched: 283416 seqs, 96216763 residues

Word size: 8

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: PIR-80.*

1: p1r1.*
2: p1r2.*
3: p1r3.*
4: p1r4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9	1.1	595	2	B97866
2	9	1.1	621	2	T11976
3	9	1.1	1381	1	S45781
4	8	1.0	125	2	A86789
5	8	1.0	136	2	C71328
6	8	1.0	152	2	A97003
7	8	1.0	250	2	S56156
8	8	1.0	308	2	S44818
9	8	1.0	359	2	A70978
10	8	1.0	418	2	E86871
11	8	1.0	420	2	S51492
12	8	1.0	448	2	S50622
13	8	1.0	461	2	H81319
14	8	1.0	495	2	H84359
15	8	1.0	689	2	E69135
16	8	1.0	795	2	AE0705
17	8	1.0	1252	2	T14272
18	8	0.9	66	2	T28235
19	8	0.9	83	2	JC5745
20	8	0.9	111	2	S03304
21	8	0.9	113	2	C90083
22	8	0.9	114	2	B87339
23	8	0.9	132	2	H72632
24	8	0.9	133	2	B69279
25	8	0.9	135	2	T02391
26	8	0.9	136	2	H82787
27	8	0.9	139	2	T49650
28	8	0.9	144	2	T01823
29	7	0.9	156	1	R3XT7

30	7	0.9	158	2	G90332	hypothetical prote
31	7	0.9	168	2	B69776	hypothetical prote
32	7	0.9	176	2	F72430	MDP-reducing hydr
33	7	0.9	184	2	F89839	ribosome recycling
34	7	0.9	189	2	G84451	probable cold-regu
35	7	0.9	193	2	H84958	phosphoprotease iso
36	7	0.9	193	2	AH2372	hypothetical prote
37	7	0.9	195	2	AE2755	conserved hypothet
38	7	0.9	198	2	C82357	transcription regu
39	7	0.9	209	2	H69901	general stress pro
40	7	0.9	215	2	E96533	hypothetical prote
41	7	0.9	218	2	D97536	hypothetical prote
42	7	0.9	229	2	JC7308	cellulase (EC 3.2.
43	7	0.9	231	2	D87715	carboxymethylendu
44	7	0.9	237	2	A84957	N-acetylmutamoyl-L
45	7	0.9	239	2	AE0772	probable exported

ALIGNMENTS

RESULT 1
B97866
DNA primase (EC 2.7.7.-) [imported] - Rickettsia conorii (strain Malish 7)
C/Species: Rickettsia conorii
C/Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
R/Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; f
Science 293, 2093-2098, 2001
A/Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A/Reference number: A97700; MUID:21442074; PMID:11557893
A/Accession: B97866
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-595 <KOR>
A/Cross-references: UNIPROT:Q92FZ7; UNIPARC:UPI00000CC08A; GB:AE006914; PIDN:AAL03868.1
C/Genetics:
A/Gene: dnag
A/Supfamily: DNA primase
C/Keywords: nucleotidyltransferase

Query Match 1.1% Score 9; DB 2; Length 595;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 KEIKIANE 94
Db 573 KEIKIANE 581

RESULT 2
T11976
glutamine-fructose-6-phosphate transaminase (isomerizing) (EC 2.6.1.16) [similarity] -
C/Species: chloroplast Cyanidium caldarium
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
R/Gloeckner, G.; Rosenthal, A.; Valentin, K.
submitted to the EMBL Data Library, September 1997
A/Description: Organisation of 46 kb of the Cyanidium caldarium RK1 plastid genome.
A/Reference number: 217374
A/Accession: T11976
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-621 <GLO>
A/Cross-references: UNIPROT:O19908; UNIPARC:UPI0000163753; EMBL:AF022186; NID:g2465730;
A/Experimental source: strain RK1
C/Genetics:
A/Gene: chlroplast
A/Note: geaa
C/Supfamily: glutamine-fructose-6-phosphate aminotransferase (isomerizing)
C/Keywords: aminotransferase; chloroplast; isomerase
F/2-621/Product: glutamine-fructose-6-phosphate transaminase (isomerizing) #status pred
F/2/Active site: Cys #status predicted

Query Match 1.1%; Score 9; DB 2; Length 621;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

141 LSKOLKEIS 149
|||||
470 LSKOLKEIS 478

DB 470 LSKOLKEIS 478

RESULT 3
S45781
probable calcium-binding protein YBL047C - yeast (Saccharomyces cerevisiae)
N/Alternate names: hypothetical protein YBL0520
C/Species: Saccharomyces cerevisiae
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C/Accession: S45781; S50284; S45782; S39841; S37339; S42498
R/Goffeau, A.; Jonniaux, J.L.; Purnelle, B.; Skala, J.; de Wergifosse, P.; van Dyck, L.
submitted to the Protein Sequence Database, August 1994
A/Reference number: S45745
A/Accession: S45781
A/Molecule type: DNA
A/Residues: 1-961 <COF>
A/Cross-references: UNIPROT:P34216; UNIPARC:UPI0000174C49; EMBL:Z35808; GSPDB:GN00002; N
A/Experimental source: strain S288C
R/de Wergifosse, P.; Jacques, B.; Jonniaux, J.L.; Purnelle, B.; Skala, J.; Goffeau, A.
Yeast 10, 1489-1496, 1994
A/Title: The sequence of a 22.4 kb DNA fragment from the left arm of yeast chromosome II
NA-binding protein.
A/Reference number: S50284; MUID:95176707; PMID:7871888
A/Accession: S50284
A/Molecule type: DNA
A/Residues: 1-961 <DEF>
A/Cross-references: UNIPARC:UPI0000174C49; EMBL:X78214
A/Experimental source: strain S288C
R/Dubois, E.; El Bakoury, M.; Glansdorff, N.; Messenguy, F.; Pierard, A.; Scherens, B.;
submitted to the Protein Sequence Database, August 1994
A/Reference number: S45782
A/Accession: S45782
A/Molecule type: DNA
A/Residues: 579-1381 <DOB>
A/Cross-references: UNIPARC:UPI0000168C7F; EMBL:Z35808; GSPDB:GN00002; MIPS:YBL047C
R/Scherens, B.; el Bakoury, M.; Vlerendael, F.; Dubois, E.; Messenguy, F.
Yeast 9, 1355-1371, 1993
A/Title: Sequencing and functional analysis of a 32 560 bp segment on the left arm of ye
A/Reference number: S39824; MUID:94205266; PMID:8154187
A/Accession: S39841
A/Molecule type: DNA
A/Residues: 579-1381 <SCH>
A/Cross-references: UNIPARC:UPI0000168C7F; EMBL:Z23261; NID:G313733; PIDN:CAA80797.1; PI
A/Experimental source: strain S288C
C/Genetics:
A/Gene: SGD:EDL1; MIPS:YBL047C
A/Cross-references: SGD:S0000143
A/Map position: 2L
C/Superfamily: Yeast probable calcium-binding protein YBL047C; calmodulin repeat homolog
C/Keywords: calcium binding; EF hand; transmembrane protein
F.167-199/Domain: calmodulin repeat homology <EF1>
F.560-576/Domain: transmembrane #status predicted <TM>

Query Match 1.1%; Score 9; DB 1; Length 1381;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

68 NSINDLLA 76
|||||
421 NSINDLLA 429

DB 421 NSINDLLA 429

RESULT 4
A86789
hypothetical protein yneH [imported] - Lactococcus lactis subsp. lactis (strain IL1403)

C/Species: Lactococcus lactis subsp. lactis
C/Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C/Accession: A86789
R/Bolotin, A.; Wincker, P.; Mauger, S.; Jallou, O.; Malarme, K.; Weisenbach, J.; Ehrh
Genome Res. 11, 731-753, 2001
A/Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
A/Reference number: A86625; MUID:21235186; PMID:1137471
A/Accession: A86789
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-125 <STO>
A/Cross-references: UNIPROT:Q9CFZ8; UNIPARC:UPI000006A07; GB:AE005176; PID:G12724292; I
A/Experimental source: strain IL1403
C/Genetics:
A/Gene: yneH

Query Match 1.0%; Score 8; DB 2; Length 125;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

50 ILKNQOLL 57
|||||
89 ILKNQOLL 96

DB 89 ILKNQOLL 96

RESULT 5
C71328
probable flagellar basal-body rod protein (flgB) - syphilis spirochete
C/Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C/Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C/Accession: C71328
R/Frazer, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwi
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDe
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A/Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A/Reference number: A71250; MUID:98332770; PMID:9665876
A/Accession: C71328
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-136 <COL>
A/Cross-references: UNIPROT:O83411; UNIPARC:UPI00000D3249; GB:AE001218; GB:AE000520; NIT
A/Experimental source: strain Nichols
C/Genetics:
A/Gene: TP0396
C/Superfamily: rod protein flgB

Query Match 1.0%; Score 8; DB 2; Length 136;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

433 LRYEVTAN 440
|||||
20 LRYEVTAN 27

DB 20 LRYEVTAN 27

RESULT 6
A97003
probable beta-D-galactosidase [imported] - Clostridium acetobutylicum
C/Species: Clostridium acetobutylicum
C/Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C/Accession: A97003
R/Nolling, U.; Breton, G.; Onelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J.; Daly, M.U.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A/Reference number: A96900; MUID:21359325; PMID:21359325
A/Accession: A97003
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-152 <KUR>
A/Cross-references: UNIPROT:Q97KTO; UNIPARC:UPI00000C9PD0; GB:AE001437; PIDN:AAK78812.1,
A/Experimental source: Clostridium acetobutylicum ATCC824

C:Genetics:
A:Gene: CAC0836

Query Match 1.0%; Score 8; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 596 IQYIVKKG 603
|||
Db 72 IQYIVKKG 79

RESULT 7

S56156
Rieske iron-sulfur protein soxP - Sulfolobus acidocaldarius
N:Alternate names: Rieske iron-sulfur protein II
C:Species: Sulfolobus acidocaldarius
C>Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C:Accession: S56156; S56173

R:Castresana, J.; Luebben, M.; Saraste, M.
J. Mol. Biol. 250, 202-210, 1995

A:Title: New archaebacterial genes coding for redox proteins: implications for the evolution of the iron-sulfur cluster

A:Reference number: S56155; MUID:95333177; PMID:7608970

A:Accession: S56156
A:Status: nucleic acid sequence not shown

A:Residues: 1-250 <CAS>
A:Molecule type: DNA

A:Cross-references: UNIPROT:Q53766; UNIPARC:UPI0000062706; EMBL:Z48338; NID:9927521; PIR:J01401

A:Accession: S56173
A:Molecule type: protein

A:Residues: 1-24 <CAZ>
A:Cross-references: UNIPARC:UPI000017A86

C:Species: Caenorhabditis elegans
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S44818

R:Anderson, K.
submitted to the EMBL Data Library, September 1993

A:Description: Sequence of the C. elegans cosmid F44B2.

A:Reference number: S44816
A:Accession: S44818

A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1308 <AND>
A:Cross-references: UNIPROT:P34438; UNIPARC:UPI000013B7D5; EMBL:L23646; NID:9388595; PIR:J01401

A:introns: 37/3; 103/3; 242/2

Query Match 1.0%; Score 8; DB 2; Length 308;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 363 KDSIAVLK 370
|||
Db 204 KDSIAVLK 211

RESULT 8

S44818
F44B2.8 protein - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S44818

R:Anderson, K.
submitted to the EMBL Data Library, September 1993

A:Description: Sequence of the C. elegans cosmid F44B2.

A:Reference number: S44816
A:Accession: S44818

A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1308 <AND>
A:Cross-references: UNIPROT:P34438; UNIPARC:UPI000013B7D5; EMBL:L23646; NID:9388595; PIR:J01401

A:introns: 37/3; 103/3; 242/2

Query Match 1.0%; Score 8; DB 2; Length 308;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 363 KDSIAVLK 370
|||
Db 204 KDSIAVLK 211

RESULT 9

A70978
probable rmlA2 protein - Mycobacterium tuberculosis (strain H37Rv)
C:Species: Mycobacterium tuberculosis
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: A70978

R:Coile, S.T.; Broesch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, J.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998

A:Authors: Squares, R.; Sulterson, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A:Reference number: A70500; MUID:98295987; PMID:9634230

A:Accession: A70978
A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
A:Residues: 1-359 <COL>

A:Cross-references: UNIPROT:P96869; UNIPARC:UPI000005ECC; GB:Z92771; GB:AL123456; NID:9388595; PIR:J01401

A:Experimental source: strain H37Rv
C:Genetics:

A:Gene: rmlA2
C:Superfamily: mannose-1-phosphate guanylyltransferase

Query Match 1.0%; Score 8; DB 2; Length 359;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 133 ALGQITLY 140
|||
Db 74 ALGQITLY 81

RESULT 10

E86871
proteolase [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C:Species: Lactococcus lactis subsp. lactis
C>Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C:Accession: E86871

R:Bohlool, A.; Winkler, P.; Mauger, S.; Jallion, O.; Malarme, K.; Weissenbach, J.; Ehrl
Genome Res. 11, 731-753, 2001

A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s

A:Reference number: A86625; MUID:21235186; PMID:11337471

A:Accession: E86871
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-418 <STO>

A:Cross-references: UNIPROT:Q9CE72; UNIPARC:UPI000006CB77; GB:AE005176; PIR:G12725016; NID:9388595; PIR:J01401

A:Experimental source: strain IL1403
C:Genetics:

A:Gene: yuef

Query Match 1.0%; Score 8; DB 2; Length 418;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 252 SEIIAKEN 259
|||
Db 163 SEIIAKEN 170

RESULT 11

S51492
48.7K intron protein - fungus (Sclerotinia sclerotiorum) mitochondrion
C:Species: mitochondrion Sclerotinia sclerotiorum
C>Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
C:Accession: S51492

R:Carbone, I.; Anderson, J.B.; Kohn, L.M.
Curr. Genet. 27, 166-176, 1995

A:Title: A group-I intron in the mitochondrial small subunit ribosomal RNA gene of Scler

A:Reference number: S51492; MUID:95308539; PMID:7788720

A:Accession: S51492
A:Molecule type: DNA

A:Residues: 1-420 <CAR>
A:Cross-references: UNIPROT:Q35928; UNIPARC:UPI0000097183; EMBL:U07553; NID:9466463; PIR:J01401

A:introns: 37/3; 103/3; 242/2

Query Match 1.0%; Score 8; DB 2; Length 418;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 252 SEIIAKEN 259
|||
Db 163 SEIIAKEN 170

RESULT 12

S51492
48.7K intron protein - fungus (Sclerotinia sclerotiorum) mitochondrion
C:Species: mitochondrion Sclerotinia sclerotiorum
C>Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
C:Accession: S51492

R:Carbone, I.; Anderson, J.B.; Kohn, L.M.
Curr. Genet. 27, 166-176, 1995

A:Title: A group-I intron in the mitochondrial small subunit ribosomal RNA gene of Scler

A:Reference number: S51492; MUID:95308539; PMID:7788720

A:Accession: S51492
A:Molecule type: DNA

A:Residues: 1-420 <CAR>
A:Cross-references: UNIPROT:Q35928; UNIPARC:UPI0000097183; EMBL:U07553; NID:9466463; PIR:J01401

A:introns: 37/3; 103/3; 242/2

A:Experimental source: host Brassica napus
C:Genetics:
A:Genome: mitochondrion
A:Genetic code: SGC3
C:Keywords: mitochondrion

Query Match 1.0%; Score 8; DB 2; Length 420;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 306 MNEHLNKE 313
|||||
DB 241 MNEHLNKE 248

RESULT 12

S50622
Hypothetical protein YERL19C - yeast (Saccharomyces cerevisiae)

C:Species: Saccharomyces cerevisiae

C>Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 09-Jul-2004

C:Accession: S50622; S57257

R:Dieterich, F.S.

submitted to the EMBL Data Library, December 1994

A:Description: The sequence of S. cerevisiae cosmids 9781, 8198, 9115, 9981, and lambda

A:Reference number: S50437

A:Accession: S50622

A:Molecule type: DNA

A:Residues: 1-448 <DIE>

A:Cross-references: UNIPROT:P40074; UNIPARC:UPI000013ACBF; EMBL:U18916; NID:G1384128; PI

R:Berteroan, R.W.; Hampsey, M.

Yeast 11, 761-766, 1995

A>Title: Sequence, map position and genome organization of the RPL17B gene, encoding rib

A:Reference number: S57256; NID:9537553; PMID:7668045

A:Accession: S57257

A>Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 270-448 <BER>

A:Cross-references: UNIPARC:UPI00001689F3; EMBL:U15653; NID:G642467; P1DN:AAA61905.1; PI

C:Genetics:

A:Cross-references: SGD:S0000921

A:Map position: 5R

C:Superfamily: Saccharomyces cerevisiae probable membrane protein YBL089w

Query Match

1.0%; Score 8; DB 2; Length 448;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 428 KKLSLRY 435
|||||

DB 141 KKLSLRY 148

RESULT 13

H81319
probable ADP-heptose synthase Cj1150C [imported] - Campylobacter jejuni (strain NCTC 111

C:Species: Campylobacter jejuni

C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C:Accession: H81319

R:Parkhill, J.; Wren, B.W.; Mungall, K.; Kelsey, J.M.; Churcher, C.; Basham, D.; Chilling

C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell

Nature 403, 665-668, 2000

A>Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyl

A:Reference number: A81250; NID:20150912; PMID:10688204

A:Accession: H81319

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-461 <PAR>

A:Cross-references: UNIPROT:Q9PNB5; UNIPARC:UPI00000C1E38; GB:AL139077; GB:AL111168; NID

C:Experimental source: serotype O2, strain NCTC 11168

C:Genetics:

A:Gene: waaB; Cj1150C

C:Superfamily: hypothetical protein b3052

Query Match 1.0%; Score 8; DB 2; Length 461;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 542 NIEGENTLE 549
|||||

DB 203 NIEGENTLE 210

RESULT 14

H84359
threonine dehydratase [imported] - Halobacterium sp. NRC-1

C:Species: Halobacterium sp. NRC-1

C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C:Accession: H84359

R:Ng, W.V.; Kennedy, S.P.; Mahapatra, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Laaky, S.

; Leithauer, B.; Keller, K.; Cruz, R.; Dawson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabc

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Edhardt, H.; Lowe, T.M.; Li

A>Title: Genome sequence of Halobacterium species NRC-1.

A:Reference number: A84160; NID:20504483; PMID:11016950

A:Accession: H84359

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-495 <STO>

A:Cross-references: UNIPROT:Q9HNM6; UNIPARC:UPI0000063A49; GB:AE004437; NID:G10581515; E

C:Genetics:

A:Gene: tluA

Query Match

1.0%; Score 8; DB 2; Length 495;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 GSLINDILA 76
|||||

DB 423 GSLINDILA 430

RESULT 15

E69135
coenzyme P420-reducing hydrogenase, beta subunit homolog - Methanobacterium thermoautotr

C:Species: Methanobacterium thermoautotrophicum

C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 05-Oct-2004

C:Accession: E69135

R:Smith, D.R.; Doucette-Stamm, L.A.; Delonghery, C.; Lee, H.; Dubois, J.; Aldredge, T.;

; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N

J. Bacteriol. 179, 7135-7155, 1997

A>Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct

A:Reference number: A69000; NID:98037514; PMID:9371463

A:Accession: E69135

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-689 <MTH>

A:Cross-references: UNIPROT:Q26380; UNIPARC:UPI0000066710; GB:AE000813; GB:AE000666; NID

A:Experimental source: strain Delta H

C:Genetics:

A:Gene: MTH280

F/78-132/Domain: ferredoxin 2[4Fe-4S] homology <FER>

Query Match 1.0%; Score 8; DB 2; Length 669;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 247 ALKTASEL 254
|||||

DB 211 ALKTASEL 218

Search completed: May 15, 2006, 20:56:25
Job time : 46 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: May 15, 2006, 20:48:41 ; Search time 232 Seconds
(without alignments)
2390.281 Million cell updates/sec

Title: US-10-698-096-17
Perfect score: 786
Sequence: 1 MOKNKLXVXALPSPIDYFN.....VELSRASSRGVINGPFSIK 786

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size: 1

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : UniProt_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	5.9	787	2	Q5JZY8_BACTU
2	43	5.5	166	2	Q93D76_BACTU
3	43	5.5	190	2	Q93D74_BACTU
4	43	5.5	786	2	Q5JZY9_BACTU
5	43	5.5	788	2	Q5JZ20_BACTU
6	43	5.5	789	2	Q69270_BACTU
7	43	5.5	789	2	Q5XPO5_BACTU
8	43	5.5	789	2	Q79SG2_BACTU
9	43	5.5	789	2	Q8R825_BACTU
10	43	5.5	789	2	Q58173_BACTU
11	43	5.5	789	2	Q58X12_BACTU
12	43	5.5	789	2	Q93821_BACTU
13	43	5.5	789	2	Q4VY70_BACTU
14	43	5.5	789	2	Q4VYF5_BACTU
15	37	4.7	789	2	Q4U3R4_BACTU
16	35	4.5	121	2	Q6S549_BACTU
17	35	4.5	136	2	Q6S547_BACTU
18	35	4.5	140	2	Q6S550_BACTU
19	35	4.5	147	2	Q6S551_BACTU
20	35	4.5	657	2	Q93D79_BACTU
21	35	4.5	789	2	Q45792_BACTU
22	32	4.1	789	2	Q45793_BACTU
23	29	3.7	175	2	Q93D75_BACTU
24	29	3.7	183	2	Q93D77_BACTU
25	29	3.7	789	2	Q71512_BACTU
26	29	3.7	803	2	Q5PXG4_BACTU
27	27	3.4	80	2	Q6S548_BACTU
28	9	1.1	595	2	Q7PA69_RICST
29	9	1.1	595	2	Q4UUT0_RICST
30	9	1.1	595	2	Q92F27_RICCN
31	9	1.1	620	1	GLMS_CVACA

32	9	1.1	1381	1	YBE7_YEAST	P34216 baccharomyc
33	9	1.1	1803	2	Q4QGV8_LEIMA	Q4QGV8 leishmania
34	9	1.0	3753	2	Q846W6_STRCM	Q846W6 streptomyc
35	8	1.0	94	2	Q722A3_LISMF	Q722A3 listeria mo
36	8	1.0	111	2	Q9K5C4_CORGL	Q9K5C4 corynebacte
37	8	1.0	111	2	Q91AK8_CORGL	Q91AK8 corynebacte
38	8	1.0	125	2	Q9CFZ8_LACLA	Q9CFZ8 lactococcu
39	8	1.0	130	2	Q4HG95_CAMCO	Q4HG95 campylobact
40	8	1.0	136	2	Q83411_TREPA	Q83411 treponema p
41	8	1.0	149	2	Q701X6_PCREN	Q701X6 uncultured
42	8	1.0	152	2	Q97KT0_CLOAB	Q97KT0 clostridium
43	8	1.0	239	2	Q50154_STRBO	Q50154 streptococc
44	8	1.0	242	1	YLS8_CABEL	P34438 caenorhabdi
45	8	1.0	250	2	Q53766_SULAC	Q53766 sulfobolus

ALIGNMENTS

RESULT 1
ID Q5JZY8_BACTU PRELIMINARY; PRT; 787 AA.
AC Q5JZY8;
DT 10-MAY-2005 (TREMBlrel. 30, Created)
DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)
DE Isp3c protein.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1428;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Van Rie J., Arnaut G., Boets A., Damme N.;
RT "Genes encoding insecticidal secreted proteins from Bacillus thuringiensis.";
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ872072; CAI43277.1; -; Genomic DNA.
DR GO: GO:0016798; P:hydrolase activity; acting on glycosyl bonds; IEA.
DR GO: GO:0016491; P:oxidoreductase activity; IEA.
DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro: IPR003305; CBM Cenc.
DR Pfam: PF02018; CBM_4_9; I.
KW Oxidoreductase.
SQ SEQUENCE 787 AA; 88359 MW; 0B1AF7876FF30D62 CRC64;
Query Match 5.9%; Score 46; DB 2; Length 787;
Best Local Similarity 100.0%; Pred. No. 2e-37;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 514 LLAITDSNKKETKLVPPNGFISNIIVENGNIENGLFEPWKANTONAY 559
Db 515 LLAITDSNKKETKLVPPNGFISNIIVENGNIENGLFEPWKANTONAY 560
RESULT 2
ID Q93D76_BACTU PRELIMINARY; PRT; 166 AA.
AC Q93D76;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Insecticidal protein Vip3a (fragment).
GN Name=Vip3a;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1428;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Loguercio L.L., Barreto M.R., Rocha T.L., Lana U.G.P., Pativa E.;
Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

RN [2]
RT NUCLEOTIDE SEQUENCE.
RC STRAIN=474L;
RA Loguercio L.L., Barreto M.R., Rocha T.L., Santos C.G., Teixeira F.F.,
RA Paiva E.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF399670; AAK97485.1; -; Genomic_DNA.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 166 AA; 18517 MW; D76BDAB1C2EF170 CRC64;

Query Match 5.5%; Score 43; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 6.4e-35;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 KTSGEVGNVNFLLVLTALQAKAFLLTTTCRKLGLADIDYT 303
DB 55 KTSGEVGNVNFLLVLTALQAKAFLLTTTCRKLGLADIDYT 97

RESULT 3

Q93D74_BACTU
ID Q93D74_BACTU PRELIMINARY; PRT; 190 AA.
AC Q93D74;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Insecticidal protein Vip3A (Fragment).
GN Name=vip3A;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1428;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=1165A;
RA Loguercio L.L., Barreto M.R., Rocha T.L., Lana U.G.P., Paiva E.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RC NUCLEOTIDE SEQUENCE.
RC STRAIN=1165A;
RA Loguercio L.L., Barreto M.R., Rocha T.L., Santos C.G., Teixeira F.F.,
RA Paiva E.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF399673; AAK97487.1; -; Genomic_DNA.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 190 AA; 21007 MW; 2D7D9377CE3647B1 CRC64;

Query Match 5.5%; Score 43; DB 2; Length 190;
Best Local Similarity 100.0%; Pred. No. 7.2e-35;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 KTSGEVGNVNFLLVLTALQAKAFLLTTTCRKLGLADIDYT 303
DB 68 KTSGEVGNVNFLLVLTALQAKAFLLTTTCRKLGLADIDYT 110

RESULT 4

Q5JZY9_BACTU
ID Q5JZY9_BACTU PRELIMINARY; PRT; 786 AA.
AC Q5JZY9;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Iap3b protein.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1428;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Van Rie J., Arnaut G., Boets A., Damme N.;

RT "Genes encoding insecticidal secreted proteins from Bacillus
RT thuringiensis.";
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ872071; CA143276.1; -; Genomic_DNA.
DR GO: GO:0016798; Fihydroxylase activity, acting on glycosyl bonds; IEA.
DR GO: GO:0016491; Fihydroxylase activity; IEA.
DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro: IPR003305; CBM_Cenc.
DR Pfam: PF02018; CBM_4_9; I.
KW Oxidoreductase.
SQ SEQUENCE 786 AA; 88997 MW; B67FD67CBA56A57 CRC64;

Query Match 5.5%; Score 43; DB 2; Length 786;
Best Local Similarity 100.0%; Pred. No. 2.4e-34;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 KTSGEVGNVNFLLVLTALQAKAFLLTTTCRKLGLADIDYT 303
DB 262 KTSGEVGNVNFLLVLTALQAKAFLLTTTCRKLGLADIDYT 304

RESULT 5

Q5JZ20_BACTU
ID Q5JZ20_BACTU PRELIMINARY; PRT; 788 AA.
AC Q5JZ20;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Iap3a protein.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1428;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Van Rie J., Arnaut G., Boets A., Damme N.;
RL "Genes encoding insecticidal secreted proteins from Bacillus
RT thuringiensis.";
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ872070; CA143275.1; -; Genomic_DNA.
DR GO: GO:0016798; Fihydroxylase activity, acting on glycosyl bonds; IEA.
DR GO: GO:0016491; Fihydroxylase activity; IEA.
DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro: IPR003305; CBM_Cenc.
DR Pfam: PF02018; CBM_4_9; I.
KW Oxidoreductase.
SQ SEQUENCE 788 AA; 88037 MW; 5A7314A1D4A60B8 CRC64;

Query Match 5.5%; Score 43; DB 2; Length 788;
Best Local Similarity 100.0%; Pred. No. 2.4e-34;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 KTSGEVGNVNFLLVLTALQAKAFLLTTTCRKLGLADIDYT 303
DB 262 KTSGEVGNVNFLLVLTALQAKAFLLTTTCRKLGLADIDYT 304

RESULT 6

O69270_BACTU
ID O69270_BACTU PRELIMINARY; PRT; 789 AA.
AC O69270;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Vegetative insecticidal protein.
GN Name=vip-s;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1428;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=A13; TISSUE=Leaf;

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RX MEDLINE=21579339; PubMed=11722946;
RX DOI=10.1128/AEM.67.12.5855-5858.2001;
RA Selvapandian A., Arora N., Rajagopal R., Jalali S.K., Venkatesan T.,
RA Singh S.P., Bhannagar R.K.;
RT "Toxicity analysis of N- and C-terminus-deleted vegetative
RT insecticidal protein from Bacillus thuringiensis.";
RL Appl. Environ. Microbiol. 67:5855-5858(2001).
DR EMBL: Y17158; CAA7665.1; -; Genomic DNA.
DR GO: GO:0016491; F:oxidoreductase activity; IEA.
DR InterPro: IPR003305; CBM_Cenc.
DR Pfam: PF02018; CBM_4_9; 1.
KW Oxidoreductase.
SQ SEQUENCE 789 AA; 88599 MW; 70619EAB6823C7AC CRC64;

Query Match 5.5%; Score 43; DB 2; Length 789;
Best Local Similarity 100.0%; Pred. No. 2.4e-34;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 KTSGEVGNVNFILVITLQAQAFLLTTCRKLGLADIDYT 303
DB 262 KTSGEVGNVNFILVITLQAQAFLLTTCRKLGLADIDYT 304

RESULT 7
Q5XP05_BACTU
ID Q5XP05_BACTU PRELIMINARY; PRT; 789 AA.
AC Q5XP05;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Vip3A.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1428;
RX [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NY-197;
RA Li J., Yan J., Yuan Z.;
RT "Cloning and expression of vip3A gene from Bacillus thuringiensis
RT strain NY-197.";
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY743436; AAU89707.1; -; Genomic DNA.
DR GO: GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO: GO:0016491; F:oxidoreductase activity; IEA.
DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro: IPR003305; CBM_Cenc.
DR Pfam: PF02018; CBM_4_9; 1.
KW Oxidoreductase.
SQ SEQUENCE 789 AA; 88642 MW; 6322FD4A4BEC70D4 CRC64;

Query Match 5.5%; Score 43; DB 2; Length 789;
Best Local Similarity 100.0%; Pred. No. 2.4e-34;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 KTSGEVGNVNFILVITLQAQAFLLTTCRKLGLADIDYT 303
DB 262 KTSGEVGNVNFILVITLQAQAFLLTTCRKLGLADIDYT 304

RESULT 8
Q7SGS2_BACTU
ID Q7SGS2_BACTU PRELIMINARY; PRT; 789 AA.
AC Q7SGS2;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Vegetative insecticidal protein.
GN Name=Vi83;
OS Bacillus thuringiensis serovar lewisii.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=169759;

```

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RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=YBT-833;
RA Cai Q., Liu Z., Sun M., Yu Z.;
RT "Vegetative insecticidal protein gene vip83 from Bacillus
RT thuringiensis serovar lewisii strain YBT-833.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY044227; AAK95326.1; -; Genomic DNA.
DR GO: GO:0016491; F:oxidoreductase activity; IEA.
DR InterPro: IPR003305; CBM_Cenc.
DR Pfam: PF02018; CBM_4_9; 1.
KW Oxidoreductase.
SQ SEQUENCE 789 AA; 88671 MW; 9DD746486823C7AE CRC64;

Query Match 5.5%; Score 43; DB 2; Length 789;
Best Local Similarity 100.0%; Pred. No. 2.4e-34;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 KTSGEVGNVNFILVITLQAQAFLLTTCRKLGLADIDYT 303
DB 262 KTSGEVGNVNFILVITLQAQAFLLTTCRKLGLADIDYT 304

RESULT 9
Q8RSZ5_BACTU
ID Q8RSZ5_BACTU PRELIMINARY; PRT; 789 AA.
AC Q8RSZ5;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Vip3A (Vip184).
GN Name=Vip3A;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1428;
RX [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=S184;
RX MEDLINE=22744951; PubMed=12859763;
RX DOI=10.1046/j.1365-2672.2003.01977.x;
RA Chen J., Yu J., Tang L., Tang M., Shi Y., Pang Y.;
RT "Comparison of the expression of Bacillus thuringiensis full-length
RT and N-terminally truncated vip3A gene in Escherichia coli.";
RL J. Appl. Microbiol. 95:310-316(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=S184;
RX PubMed=12674638;
RA Chen J.W., Tang L.X., Tang M.J., Shi Y.X., Pang Y.;
RT "[Cloning and expression product of vip3A gene from Bacillus
RT thuringiensis and analysis of insecticidal activity].";
RL Sheng Wu Gong Cheng Xue Bao 18:687-692(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Chen J., Yu J., Pang Y.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY074706; AAL69542.1; -; Genomic DNA.
DR EMBL: AY187679; AAO32350.1; -; Genomic DNA.
DR GO: GO:0016491; F:oxidoreductase activity; IEA.
DR InterPro: IPR003305; CBM_Cenc.
DR Pfam: PF02018; CBM_4_9; 1.
KW Oxidoreductase.
SQ SEQUENCE 789 AA; 88645 MW; D9DF334011551472 CRC64;

Query Match 5.5%; Score 43; DB 2; Length 789;
Best Local Similarity 100.0%; Pred. No. 2.4e-34;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 KTSGEVGNVNFILVITLQAQAFLLTTCRKLGLADIDYT 303
DB 262 KTSGEVGNVNFILVITLQAQAFLLTTCRKLGLADIDYT 304

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RESULT 10
Q58133_BACTU PRELIMINARY; PRT; 789 AA.
ID Q58133_BACTU PRELIMINARY; PRT; 789 AA.
AC Q58133_
DT 10-MAY-2005 (TREMBlrel. 30, Created)
DT 10-MAY-2005 (TREMBlrel. 30, last sequence update)
DE Vegetative insecticidal protein.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1428;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=9816C;
RA Cai J., Xiao L.;
RT "Bacillus thuringiensis strain 9816C vegetative insecticidal protein
gene."
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY945939; AAX49395.1; -; Genomic_DNA.
KW Oxidoreductase.
SQ SEQUENCE 789 AA; 88675 MW; 9F13448EAAE7C7AA CRC64;

Query Match 5.5%; Score 43; DB 2; Length 789;
Best Local Similarity 100.0%; Pred. No. 2.4e-34;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 KTSGSEGVNVPFLIVTLALQAKAFLLTTCRKLGLADIDYT 303
DB 262 KTSGSEGVNVPFLIVTLALQAKAFLLTTCRKLGLADIDYT 304

RESULT 11
Q58X12_BACTU PRELIMINARY; PRT; 789 AA.
ID Q58X12_BACTU PRELIMINARY; PRT; 789 AA.
AC Q58X12;
DT 10-MAY-2005 (TREMBlrel. 30, Created)
DT 10-MAY-2005 (TREMBlrel. 30, last sequence update)
DT 10-MAY-2005 (TREMBlrel. 30, last annotation update)
DE Vegetative insecticidal protein.
GN Name=vip3B;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1428;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Abdelkefi Mesrati L., Tounsi S., Jaoua S.;
RT "Characterization of a novel vip3-type gene from Bacillus
thuringiensis and evidence of its presence on a large plasmid."
RL FEMS Microbiol. Lett. 244:353-358(2005).
DR EMBL; AY739665; AAM65132.1; -; Genomic_DNA.
KW Oxidoreductase.
SQ SEQUENCE 789 AA; 88671 MW; ECB5355939FE76CA CRC64;

Query Match 5.5%; Score 43; DB 2; Length 789;
Best Local Similarity 100.0%; Pred. No. 2.4e-34;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 KTSGSEGVNVPFLIVTLALQAKAFLLTTCRKLGLADIDYT 303
DB 262 KTSGSEGVNVPFLIVTLALQAKAFLLTTCRKLGLADIDYT 304

RESULT 12
Q93821_BACTU PRELIMINARY; PRT; 789 AA.
ID Q93821_BACTU PRELIMINARY; PRT; 789 AA.
AC Q93821_0812N0;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, last sequence update)
DT 10-MAY-2005 (TREMBlrel. 30, last annotation update)
DE Vegetative insecticidal protein Vip3A (Vegetative insecticidal protein
```

```
DE vip3V).
GN Name=vip3A; Synonyms=vip3A-WB5, vip3V;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1428;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=6101, and 611;
RA Chen J., Yu J., Pang Y., Tang L.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Wu Y., Guan X.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=WB 50;
RX PubMed=15604775; DOI=10.1023/B:BILE.0000045645.4536.3f;
RA Wu Z.L., Guo W.Y., Qiu J.Z., Huang T.P., Li X.B., Guan X.;
RL "Cloning and localization of vip3A gene of Bacillus thuringiensis."
RT Biotechnol. Lett. 26:1425-1428(2004).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22244722; PubMed=12356474; DOI=10.1016/S1046-5928(02)00515-6;
RA Doss V.A., Anup Kumar K., Jayakumar R., Sekar V.;
RT "Cloning and expression of the vegetative insecticidal protein (vip3V)
gene of Bacillus thuringiensis in Escherichia coli."
RL Protein Expr. Purif. 26:82-88(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C9;
RA Liu R., Song F., Zhang J.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY074707; AAL69543.1; -; Genomic_DNA.
DR EMBL; AF500478; AAM22456.2; -; Genomic_DNA.
DR EMBL; AY295778; AAP51131.1; -; Genomic_DNA.
DR EMBL; AF373030; AAN60738.1; -; Genomic_DNA.
DR EMBL; AY489126; AAR36859.1; -; Genomic_DNA.
DR EMBL; AY074708; AAL69544.1; -; Genomic_DNA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
DR InterPro; IPR003305; Cenc_cabd_bd.
DR Pfam; PF02018; CBM_4_9; 1.
KW Oxidoreductase.
SQ SEQUENCE 789 AA; 88672 MW; 9DD746486623C7AE CRC64;

Query Match 5.5%; Score 43; DB 2; Length 789;
Best Local Similarity 100.0%; Pred. No. 2.4e-34;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 KTSGSEGVNVPFLIVTLALQAKAFLLTTCRKLGLADIDYT 303
DB 262 KTSGSEGVNVPFLIVTLALQAKAFLLTTCRKLGLADIDYT 304

RESULT 13
Q4VYT0_BACTU PRELIMINARY; PRT; 789 AA.
ID Q4VYT0_BACTU PRELIMINARY; PRT; 789 AA.
AC Q4VYT0;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, last annotation update)
DE Vegetative insecticidal protein.
GN Name=vip3A;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1428;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BTAB51;
RA Pham N.B., Le N.H., Pham T.T., Chu H.H., Le B.T.;
RT "Cloning and sequence analysis gene encoding the vegetative
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RT Insecticidal protein (VIP3A) of some Vietnamese *B. thuringiensis* strains."
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ971413; CA196522.1; -; Genomic_DNA.
 DR InterPro: IPR003305; Cenc_card_bd.
 DR Pfam; PF02018; CBM_4_9; 1.
 KM Oxidoreductase.
 SQ SEQUENCE 789 AA; 88614 MW; 5F255A098B9C86DD CRC64;

Query Match 5.5%; Score 43; DB 2; Length 789;
 Best Local Similarity 100.0%; Pred. No. 2.4e-34;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 KTGSGEVGNVYNNFLIVLTALQAKAFLLTTCRKLGGLADIDYT 303
 DB 262 KTGSGEVGNVYNNFLIVLTALQAKAFLLTTCRKLGGLADIDYT 304

RESULT 14

Q4U3F5_BACTU
 ID Q4U3F5_BACTU PRELIMINARY; PRT; 789 AA.
 AC Q4U3F5;
 DT 13-SEP-2005 (TREMBlrel. 31, Created)
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
 DE Vegetative insecticidal protein.
 GN Name=VIP3A;
 OS *Bacillus thuringiensis*.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
 OC *Bacillus cereus* group.
 OX NCBI_TaxID=1428;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=LS1;
 RA Lu X., Hao H., Sun S., Zhu M., Du K., Li G.,
 RT "Vegetative insecticidal protein gene vip3A-1st from *Bacillus thuringiensis* strain LS1."
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; DQ016968; AAY41427.1; -; Genomic_DNA.
 DR InterPro: IPR003305; Cenc_card_bd.
 DR Pfam; PF02018; CBM_4_9; 1.
 KM Oxidoreductase.
 SQ SEQUENCE 789 AA; 88574 MW; A82803275AFEC19C CRC64;

Query Match 5.5%; Score 43; DB 2; Length 789;
 Best Local Similarity 100.0%; Pred. No. 2.4e-34;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 KTGSGEVGNVYNNFLIVLTALQAKAFLLTTCRKLGGLADIDYT 303
 DB 262 KTGSGEVGNVYNNFLIVLTALQAKAFLLTTCRKLGGLADIDYT 304

RESULT 15

Q4U3F4_BACTU
 ID Q4U3F4_BACTU PRELIMINARY; PRT; 789 AA.
 AC Q4U3F4;
 DT 13-SEP-2005 (TREMBlrel. 31, Created)
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
 DE Vegetative insecticidal protein.
 GN Name=VIP3A;
 OS *Bacillus thuringiensis*.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
 OC *Bacillus cereus* group.
 OX NCBI_TaxID=1428;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=LS8;
 RA Lu X., Hao H., Sun S., Zhu M., Du K., Li G.,
 RT "Vegetative insecticidal protein gene vip3A-1st from *Bacillus thuringiensis* strain LS8."
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.

DR EMBL; DQ016969; AAY41428.1; -; Genomic_DNA.
 DR InterPro: IPR003305; Cenc_card_bd.
 DR Pfam; PF02018; CBM_4_9; 1.
 KM Oxidoreductase.
 SQ SEQUENCE 789 AA; 88540 MW; D4A09EDA53898B3 CRC64;

Query Match 4.7%; Score 37; DB 2; Length 789;
 Best Local Similarity 100.0%; Pred. No. 3.6e-28;
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 267 VGNVYNNFLIVLTALQAKAFLLTTCRKLGGLADIDYT 303
 DB 268 VGNVYNNFLIVLTALQAKAFLLTTCRKLGGLADIDYT 304

Search completed: May 15, 2006, 20:55:35
 Job time : 233 secs

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OM protein - protein search, using sw model

Run on: May 15, 2006, 20:55:51 ; Search time 47 Seconds
(without alignments)
1382.619 Million cell updates/sec

Title: US-10-698-096-17

Perfect score: 786
Sequence: 1 MQNNKLSVKALPSFIDYFN.....VELSRSSRGVINGDFSIK 786

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 572060 seqs, 82675679 residues

Word size: 1

Total number of hits satisfying chosen parameters: 570988

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Issued Patents AA: *
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2: /cgn2_6/ptodata/1/iaa/6.COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/H.COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PCITUS.COMB.pep.*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	5.7	787	2	US-09-307-106-54 Sequence 54, Appl
2	43	5.5	511	2	US-09-002-285-88 Sequence 88, Appl
3	43	5.5	511	2	US-09-589-477-88 Sequence 88, Appl
4	43	5.5	511	2	US-10-099-285A-88 Sequence 88, Appl
5	43	5.5	759	2	US-09-002-285-86 Sequence 86, Appl
6	43	5.5	759	2	US-09-589-477-86 Sequence 86, Appl
7	43	5.5	759	2	US-10-099-285A-86 Sequence 86, Appl
8	43	5.5	789	2	US-08-960-780-6 Sequence 6, Appl
9	43	5.5	789	2	US-09-073-898-6 Sequence 6, Appl
10	43	5.5	789	2	US-09-002-285-80 Sequence 80, Appl
11	43	5.5	789	2	US-09-002-285-82 Sequence 82, Appl
12	43	5.5	789	2	US-09-002-285-84 Sequence 84, Appl
13	43	5.5	789	2	US-09-002-285-90 Sequence 90, Appl
14	43	5.5	789	2	US-09-002-285-92 Sequence 92, Appl
15	43	5.5	789	2	US-09-002-285-94 Sequence 94, Appl
16	43	5.5	789	2	US-09-002-285-96 Sequence 96, Appl
17	43	5.5	789	2	US-09-002-285-100 Sequence 100, Appl
18	43	5.5	789	2	US-09-589-477-80 Sequence 80, Appl
19	43	5.5	789	2	US-09-589-477-82 Sequence 82, Appl
20	43	5.5	789	2	US-09-589-477-84 Sequence 84, Appl
21	43	5.5	789	2	US-09-589-477-90 Sequence 90, Appl
22	43	5.5	789	2	US-09-589-477-92 Sequence 92, Appl
23	43	5.5	789	2	US-09-589-477-94 Sequence 94, Appl
24	43	5.5	789	2	US-09-589-477-96 Sequence 96, Appl
25	43	5.5	789	2	US-09-589-477-100 Sequence 100, Appl
26	43	5.5	789	2	US-09-850-351A-6 Sequence 6, Appl
27	43	5.5	789	2	US-10-099-285A-80 Sequence 80, Appl

28	43	5.5	789	2	US-10-099-285A-82 Sequence 82, Appl
29	43	5.5	789	2	US-10-099-285A-84 Sequence 84, Appl
30	43	5.5	789	2	US-10-099-285A-90 Sequence 90, Appl
31	43	5.5	789	2	US-10-099-285A-92 Sequence 92, Appl
32	43	5.5	789	2	US-10-099-285A-94 Sequence 94, Appl
33	43	5.5	789	2	US-10-099-285A-96 Sequence 96, Appl
34	43	5.5	790	2	US-10-099-285A-100 Sequence 100, Appl
35	43	5.5	790	2	US-08-960-780-4 Sequence 4, Appl
36	43	5.5	790	2	US-08-960-780-8 Sequence 8, Appl
37	43	5.5	790	2	US-09-073-898-4 Sequence 4, Appl
38	43	5.5	790	2	US-09-073-898-8 Sequence 8, Appl
39	43	5.5	790	2	US-09-002-285-102 Sequence 102, App
40	43	5.5	790	2	US-09-589-477-102 Sequence 2, Appl
41	43	5.5	790	2	US-09-307-106-2 Sequence 2, Appl
42	43	5.5	790	2	US-09-850-351A-4 Sequence 4, Appl
43	43	5.5	790	2	US-09-850-351A-8 Sequence 8, Appl
44	43	5.5	790	2	US-10-099-285A-102 Sequence 102, App
45	41	5.2	789	2	US-09-002-285-78 Sequence 78, Appl

ALIGNMENTS

RESULT 1
US-09-307-106-54
Sequence 54, Application US/09307106
Patent No. 6603063
GENERAL INFORMATION:
APPLICANT: Feltelson, Jerald S.
APPLICANT: Schneck, H. Ernest
APPLICANT: Narva, Kenneth B.
APPLICANT: Stockhoff, Brian A.
APPLICANT: Schmeltz, James
APPLICANT: Loewer, David
APPLICANT: Dullum, Charles Joseph
APPLICANT: Muller-Cohn, Judy
APPLICANT: Stamp, Lisa
APPLICANT: Morrill, George
TITLE OF INVENTION: No. 6603063el Pesticidal Toxins and Nucleotide
TITLE OF INVENTION: Sequences Which Encode These Toxins
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: US
ZIP: 32606-6669
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09307,106
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,848
FILING DATE: 30-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/960,780
FILING DATE: 30-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/073,898
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-708C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100

TELEFAX: 352-372-5800
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 787 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-307-106-54

Query Match 5.7%; Score 45; DB 2; Length 787;
Best Local Similarity 100.0%; Pred. No. 4.3e-37;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 139 EYLSKQLEISDRLDIVINVLINSTITTEITTPAYORIKYNEKFE 183
Db 140 EYLSKQLEISDRLDIVINVLINSTITTEITTPAYORIKYNEKFE 184

RESULT 2
US-09-002-285-88
Sequence 88, Application US/09002285
Patent No. 6369213
GENERAL INFORMATION:
APPLICANT: Schnepf, H. Ernest
APPLICANT: Wicker, Carol
APPLICANT: Narva, Kenneth E.
APPLICANT: Walz, Michelle
APPLICANT: Stockhoff, Brian
APPLICANT: Muller-Cohn, Judy
TITLE OF INVENTION: Toxins Active Against Pests
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/002,285
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/886,615
FILING DATE: 1-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/674,002
FILING DATE: 1-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-701C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:
LENGTH: 511 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-002-285-88

Query Match 5.5%; Score 43; DB 2; Length 511;
Best Local Similarity 100.0%; Pred. No. 3.3e-35;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 KTSGEVGNVNFLLVLTALQAKFLTTTCRKLGLADIDYT 303
Db 122 KTSGEVGNVNFLLVLTALQAKFLTTTCRKLGLADIDYT 164

RESULT 3
US-09-589-477-88
Sequence 88, Application US/09589477
Patent No. 6570005
GENERAL INFORMATION:
APPLICANT: Schnepf, H. Ernest
APPLICANT: Wicker, Carol
APPLICANT: Narva, Kenneth E.
APPLICANT: Walz, Michelle
APPLICANT: Stockhoff, Brian
TITLE OF INVENTION: Toxins Active Against Pests
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/589,477
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/886,615
FILING DATE: 1-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/674,002
FILING DATE: 1-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-701C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:
LENGTH: 511 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-589-477-88

Query Match 5.5%; Score 43; DB 2; Length 511;
Best Local Similarity 100.0%; Pred. No. 3.3e-35;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 KTSGEVGNVNFLLVLTALQAKFLTTTCRKLGLADIDYT 303
Db 122 KTSGEVGNVNFLLVLTALQAKFLTTTCRKLGLADIDYT 164

RESULT 4
US-10-099-285A-88
Sequence 88, Application US/10099285A
Patent No. 6752992
GENERAL INFORMATION:
APPLICANT: Schnepf, H. Ernest

```

Wicker, Carol
Narva, Kenneth E.
Walz, Michelle
Stockhoff, Brian
Muller-Cohn, Judy
TITLE OF INVENTION: Toxins Active Against Pests
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/099,285A
FILING DATE: 02-Jul-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/002,285
FILING DATE: 31-DEC-1997
APPLICATION NUMBER: US 08/886,615
FILING DATE: 1-JUL-1997
APPLICATION NUMBER: US 08/674,002
FILING DATE: 1-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-701C2D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:
LENGTH: 511 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 88:
US-10-099-285A-88

Query Match      5.5%; Score 43; DB 2; Length 511;
Best Local Similarity 100.0%; Pred. No. 3.3e-35;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      261 KTSGSEGVNPNLVLTALQAKAFLLTTCRLGLADIYDT 303
DB      122 KTSGSEGVNPNLVLTALQAKAFLLTTCRLGLADIYDT 164

RESULT 5
US-09-002-285-86
Sequence 86, Application US/09002285
GENERAL INFORMATION:
APPLICANT: Schnepf, H. Ernest
APPLICANT: Wicker, Carol
APPLICANT: Narva, Kenneth E.
APPLICANT: Walz, Michelle
APPLICANT: Stockhoff, Brian
APPLICANT: Muller-Cohn, Judy
TITLE OF INVENTION: Toxins Active Against Pests
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
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STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/002,285
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/886,615
FILING DATE: 1-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/674,002
FILING DATE: 1-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-701C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 372-5800
TELEFAX: (352) 375-8100
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 759 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-002-285-86
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Query Match      5.5%; Score 43; DB 2; Length 759;
Best Local Similarity 100.0%; Pred. No. 4.8e-35;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      261 KTSGSEGVNPNLVLTALQAKAFLLTTCRLGLADIYDT 303
DB      262 KTSGSEGVNPNLVLTALQAKAFLLTTCRLGLADIYDT 304
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RESULT 6
US-09-589-477-86
Sequence 86, Application US/09589477
GENERAL INFORMATION:
APPLICANT: Schnepf, H. Ernest
APPLICANT: Wicker, Carol
APPLICANT: Narva, Kenneth E.
APPLICANT: Walz, Michelle
APPLICANT: Stockhoff, Brian
TITLE OF INVENTION: Toxins Active Against Pests
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/589,477
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/886,615
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FILING DATE: 1-JUL-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/674,002
FILING DATE: 1-JUL-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-701C1C1
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 759 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-589-477-86

Query Match 5.5%; Score 43; DB 2; Length 759;
Best Local Similarity 100.0%; Pred. No. 4.8e-35;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 KTSGSEGVNVPFLVLTALQAKAFLLTTCRKLGLADIDYT 303
DB 262 KTSGSEGVNVPFLVLTALQAKAFLLTTCRKLGLADIDYT 304

RESULT 7
US-10-099-285A-86
Sequence 86, Application US/10099285A
Patent No. 6752992
GENERAL INFORMATION:
APPLICANT: Schneck, H. Ernest
Wicker, Carol
Narva, Kenneth E.
Walz, Michelle
Stockhoff, Brian
Muller-Cohn, Judy
TITLE OF INVENTION: Toxins Active Against Pests
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/099,285A
FILING DATE: 02-Jul-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/002,285
FILING DATE: 31-DEC-1997
APPLICATION NUMBER: US 08/886,615
FILING DATE: 1-JUL-1997
APPLICATION NUMBER: US 08/674,002
FILING DATE: 1-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-701C2D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100

TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 759 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 86:
US-10-099-285A-86

Query Match 5.5%; Score 43; DB 2; Length 759;
Best Local Similarity 100.0%; Pred. No. 4.8e-35;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 KTSGSEGVNVPFLVLTALQAKAFLLTTCRKLGLADIDYT 303
DB 262 KTSGSEGVNVPFLVLTALQAKAFLLTTCRKLGLADIDYT 304

RESULT 8
US-08-960-780-6
Sequence 6, Application US/08960780
Patent No. 6204435
GENERAL INFORMATION:
APPLICANT: Feltelson, Jerald S.
APPLICANT: Schneck, H. Ernest
APPLICANT: Narva, Kenneth E.
APPLICANT: Stockhoff, Brian A.
APPLICANT: Schmeltz, James
APPLICANT: Loewer, David
APPLICANT: Dullum, Charles Joseph
APPLICANT: Muller-Cohn, Judy
APPLICANT: Stamp, Lisa
TITLE OF INVENTION: No. 6204435e1 Pesticidal Toxins and Nucleotide
TITLE OF INVENTION: Sequences which Encode These Toxins
NUMBER OF SEQUENCES: 134
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: US
ZIP: 32606-6669
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/960,780
FILING DATE: 30-OCT-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,848
FILING DATE: 30-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA-708
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
TELEFAX: 352-372-5800
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 789 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: 81Pd
US-08-960-780-6

Query Match 5.5%; Score 43; DB 2; Length 789;
Best Local Similarity 100.0%; Pred. No. 4.9e-35;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 KTSGEVGNVNFILVLTALQAKAFLLTTCRKLGLADIDYT 303
DB 262 KTSGEVGNVNFILVLTALQAKAFLLTTCRKLGLADIDYT 304

RESULT 9

US-09-073-898-6
Sequence 6, Application US/09073898
Patent No. 6242669
GENERAL INFORMATION:
APPLICANT: Petelerson, Jerald S.
APPLICANT: Schnepf, H. Ernest
APPLICANT: Narva, Kenneth E.
APPLICANT: Stockhoff, Brian A.
APPLICANT: Schmeltz, James
APPLICANT: Loewer, David
APPLICANT: Dullum, Charles Joseph
APPLICANT: Muller-Cohn, Judy
APPLICANT: Stamp, Lisa
APPLICANT: Morrill, George
APPLICANT: Finstad-Lee, Stacey
TITLE OF INVENTION: No. 624269e1 Pesticidal Toxins and Nucleotide
TITLE OF INVENTION: Sequences which Encode These Toxins
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: US
ZIP: 32606-6669
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,898
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,848
FILING DATE: 30-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/960,780
FILING DATE: 30-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-708C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
TELEFAX: 352-372-5800
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 789 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: 81F6
US-09-073-898-6

Query Match 5.5%; Score 43; DB 2; Length 789;
Best Local Similarity 100.0%; Pred. No. 4.9e-35;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 KTSGEVGNVNFILVLTALQAKAFLLTTCRKLGLADIDYT 303
DB 262 KTSGEVGNVNFILVLTALQAKAFLLTTCRKLGLADIDYT 304

RESULT 10

US-09-002-285-80
Sequence 80, Application US/09002285
Patent No. 6369213
GENERAL INFORMATION:
APPLICANT: Schnepf, H. Ernest
APPLICANT: Wicker, Carol
APPLICANT: Narva, Kenneth E.
APPLICANT: Walz, Michelle
APPLICANT: Stockhoff, Brian
APPLICANT: Muller-Cohn, Judy
TITLE OF INVENTION: Toxins Active Against Peets
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/002,285
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/886,615
FILING DATE: 1-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/674,002
FILING DATE: 1-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-701C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 789 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-002-285-80

Query Match 5.5%; Score 43; DB 2; Length 789;
Best Local Similarity 100.0%; Pred. No. 4.9e-35;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 KTSGEVGNVNFILVLTALQAKAFLLTTCRKLGLADIDYT 303
DB 262 KTSGEVGNVNFILVLTALQAKAFLLTTCRKLGLADIDYT 304

RESULT 11

US-09-002-285-82
Sequence 82, Application US/09002285
Patent No. 6369213
GENERAL INFORMATION:
APPLICANT: Schnepf, H. Ernest
APPLICANT: Wicker, Carol
APPLICANT: Narva, Kenneth E.

```

: APPLICANT: Walz, Michelle
: APPLICANT: Stockhoff, Brian
: APPLICANT: Muller-Cohn, Judy
: TITLE OF INVENTION: Toxins Active Against Pests
: NUMBER OF SEQUENCES: 105
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
: STREET: 2421 N.W. 41st Street, Suite A-1
: CITY: Gainesville
: STATE: Florida
: COUNTRY: USA
: ZIP: 32606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US 09/002,285
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/886,615
: FILING DATE: 1-JUL-1997
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/674,002
: FILING DATE: 1-JUL-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Sanders, Jay M.
: REGISTRATION NUMBER: 39,355
: REFERENCE/DOCKET NUMBER: MA-701C2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (352) 375-8100
: TELEFAX: (352) 372-5800
: INFORMATION FOR SEQ ID NO: 82:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 789 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-09-002-285-82

Query Match          5.5%; Score 43; DB 2; Length 789;
Best Local Similarity 100.0%; Pred. No. 4.9e-35;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      261 KTGSGEVGVNPLIVLTALQAKAFILTTTCRKLGLADIDYT 303
DB      262 KTGSGEVGVNPLIVLTALQAKAFILTTTCRKLGLADIDYT 304

RESULT 12
US-09-002-285-84
: Sequence 84, Application US/09002285
: Patent No. 6369213
: GENERAL INFORMATION:
: APPLICANT: Schnepf, H. Ernest
: APPLICANT: Wicker, Carol
: APPLICANT: Narva, Kenneth E.
: APPLICANT: Walz, Michelle
: APPLICANT: Stockhoff, Brian
: APPLICANT: Muller-Cohn, Judy
: TITLE OF INVENTION: Toxins Active Against Pests
: NUMBER OF SEQUENCES: 105
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
: STREET: 2421 N.W. 41st Street, Suite A-1
: CITY: Gainesville
: STATE: Florida
: COUNTRY: USA
: ZIP: 32606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US 09/002,285
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/886,615
: FILING DATE: 1-JUL-1997
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/674,002
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: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US 09/002,285
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/886,615
: FILING DATE: 1-JUL-1997
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/674,002
: FILING DATE: 1-JUL-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Sanders, Jay M.
: REGISTRATION NUMBER: 39,355
: REFERENCE/DOCKET NUMBER: MA-701C2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (352) 375-8100
: TELEFAX: (352) 372-5800
: INFORMATION FOR SEQ ID NO: 84:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 789 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-09-002-285-84

Query Match          5.5%; Score 43; DB 2; Length 789;
Best Local Similarity 100.0%; Pred. No. 4.9e-35;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      261 KTGSGEVGVNPLIVLTALQAKAFILTTTCRKLGLADIDYT 303
DB      262 KTGSGEVGVNPLIVLTALQAKAFILTTTCRKLGLADIDYT 304

RESULT 13
US-09-002-285-90
: Sequence 90, Application US/09002285
: Patent No. 6369213
: GENERAL INFORMATION:
: APPLICANT: Schnepf, H. Ernest
: APPLICANT: Wicker, Carol
: APPLICANT: Narva, Kenneth E.
: APPLICANT: Walz, Michelle
: APPLICANT: Stockhoff, Brian
: APPLICANT: Muller-Cohn, Judy
: TITLE OF INVENTION: Toxins Active Against Pests
: NUMBER OF SEQUENCES: 105
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
: STREET: 2421 N.W. 41st Street, Suite A-1
: CITY: Gainesville
: STATE: Florida
: COUNTRY: USA
: ZIP: 32606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US 09/002,285
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/886,615
: FILING DATE: 1-JUL-1997
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/674,002
```

;; FILING DATE: 1-JUL-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Sanders, Jay M.
;; REGISTRATION NUMBER: 39,355
;; REFERENCE/DOCKET NUMBER: MA-701C2
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (352) 375-8100
;; TELEFAX: (352) 372-5800
;; INFORMATION FOR SEQ ID NO: 90:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 789 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-09-002-285-90

Query Match
Best Local Similarity 100.0%; Score 43; DB 2; Length 789;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 261 KTSGSEGVNPNFLIVLTALQAKAFLLTTCRKLGLADIDYT 303
DB 262 KTSGSEGVNPNFLIVLTALQAKAFLLTTCRKLGLADIDYT 304

RESULT 14
US-09-002-285-92
; Sequence 92, Application US/09002285
; Patent No. 6369213
; GENERAL INFORMATION:
; APPLICANT: Schnepf, H. Ernest
; APPLICANT: Wicker, Carol
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Walz, Michelle
; APPLICANT: Stockhoff, Brian
; APPLICANT: Muller-Cohn, Judy
; TITLE OF INVENTION: Toxins Active Against Peests
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentlin
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/002,285
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/886,615
; FILING DATE: 1-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/674,002
; FILING DATE: 1-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: MA-701C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 789 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-09-002-285-92

Query Match
Best Local Similarity 100.0%; Score 43; DB 2; Length 789;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 261 KTSGSEGVNPNFLIVLTALQAKAFLLTTCRKLGLADIDYT 303
DB 262 KTSGSEGVNPNFLIVLTALQAKAFLLTTCRKLGLADIDYT 304

RESULT 15
US-09-002-285-94
; Sequence 94, Application US/09002285
; Patent No. 6369213
; GENERAL INFORMATION:
; APPLICANT: Schnepf, H. Ernest
; APPLICANT: Wicker, Carol
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Walz, Michelle
; APPLICANT: Stockhoff, Brian
; APPLICANT: Muller-Cohn, Judy
; TITLE OF INVENTION: Toxins Active Against Peests
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentlin
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/002,285
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/886,615
; FILING DATE: 1-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/674,002
; FILING DATE: 1-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: MA-701C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 789 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-002-285-94

Query Match
Best Local Similarity 100.0%; Score 43; DB 2; Length 789;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 261 KTSGSEGVNPNFLIVLTALQAKAFLLTTCRKLGLADIDYT 303
DB 262 KTSGSEGVNPNFLIVLTALQAKAFLLTTCRKLGLADIDYT 304

Tue May 16 14:47:42 2006

us-10-698-096-17.oli.rat

Page 8

Search completed: May 15, 2006, 20:57:18
Job time : 48 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

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Title: US-10-698-096-17

Perfect score: 786
Sequence: 1 MOKNNKLSVXALPSFIDYFN.....VELSRASSRGVINGDFSIK 786

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1866650

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Published Applications AA_Main:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	786	100.0	786	4 US-10-698-096-17	Sequence 17, App1
2	45	5.7	787	4 US-10-452-002A-54	Sequence 54, App1
3	45	5.7	787	4 US-10-698-096-25	Sequence 25, App1
4	45	5.7	788	4 US-10-698-096-27	Sequence 27, App1
5	43	5.5	511	4 US-10-099-285-88	Sequence 88, App1
6	43	5.5	759	4 US-10-099-285-86	Sequence 86, App1
7	43	5.5	786	4 US-10-698-096-19	Sequence 19, App1
8	43	5.5	787	4 US-10-473-687-2	Sequence 2, App1
9	43	5.5	787	4 US-10-473-687-7	Sequence 7, App1
10	43	5.5	787	4 US-10-505-315-7	Sequence 11, App1
11	43	5.5	788	5 US-10-505-315-11	Sequence 11, App1
12	43	5.5	788	5 US-10-505-315-32	Sequence 32, App1
13	43	5.5	789	3 US-09-850-351A-6	Sequence 6, App1
14	43	5.5	789	4 US-10-099-285-80	Sequence 80, App1
15	43	5.5	789	4 US-10-099-285-82	Sequence 82, App1
16	43	5.5	789	4 US-10-099-285-84	Sequence 84, App1
17	43	5.5	789	4 US-10-099-285-90	Sequence 90, App1
18	43	5.5	789	4 US-10-099-285-92	Sequence 92, App1
19	43	5.5	789	4 US-10-099-285-94	Sequence 94, App1
20	43	5.5	789	4 US-10-099-285-96	Sequence 96, App1
21	43	5.5	789	4 US-10-099-285-100	Sequence 100, App1
22	43	5.5	789	4 US-10-698-096-6	Sequence 6, App1
23	43	5.5	789	4 US-10-473-687-5	Sequence 5, App1
24	43	5.5	789	5 US-10-505-315-5	Sequence 5, App1
25	43	5.5	790	3 US-09-850-351A-4	Sequence 4, App1
26	43	5.5	790	3 US-09-850-351A-8	Sequence 8, App1
27	43	5.5	790	4 US-10-099-285-102	Sequence 102, App1

28	43	5.5	790	4 US-10-452-002A-2	Sequence 2, App1
29	43	5.5	790	4 US-10-698-096-4	Sequence 4, App1
30	43	5.5	790	4 US-10-698-096-8	Sequence 8, App1
31	41	5.2	789	4 US-10-099-285-78	Sequence 78, App1
32	38	4.8	788	5 US-10-505-315-2	Sequence 2, App1
33	35	4.5	789	3 US-09-904-226-2	Sequence 2, App1
34	35	4.5	789	3 US-10-099-285-98	Sequence 98, App1
35	32	4.1	789	3 US-09-904-226-4	Sequence 4, App1
36	30	3.8	746	3 US-09-904-226-6	Sequence 6, App1
37	29	3.7	801	5 US-10-505-315-9	Sequence 9, App1
38	9	1.1	1381	4 US-10-369-493-1417	Sequence 1417, App1
39	9	1.1	3753	3 US-09-980-217-29	Sequence 29, App1
40	8	1.0	72	4 US-10-425-115-312302	Sequence 312302, App1
41	8	1.0	111	3 US-09-738-626-4031	Sequence 4031, App1
42	8	1.0	359	3 US-09-712-363-269	Sequence 269, App1
43	8	1.0	461	4 US-10-282-122A-54522	Sequence 54522, App1
44	8	1.0	485	4 US-10-156-761-11034	Sequence 11034, App1
45	8	1.0	582	4 US-10-369-493-13500	Sequence 13500, App1

ALIGNMENTS

```
RESULT 1
US-10-698-096-17
; Sequence 17, Application US/10698096
; Publication No. US20040128716A1
; GENERAL INFORMATION:
; APPLICANT: Narva, Kenneth
; TITLE OF INVENTION: Polynucleotides, Pesticidal Proteins, and Novel Methods of Using
; FILE REFERENCE: NA-708C01
; CURRENT APPLICATION NUMBER: US/10/698,096
; PRIOR FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: US 09/850,351
; PRIOR FILING DATE: 2001-05-07
; PRIOR APPLICATION NUMBER: US 09/073,898
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: US 08/690,780
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 60/029,848
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 786
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-698-096-17

Query Match      100.0%; Score 786; DB 4; Length 786;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 786; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOKNNKLSVXALPSFIDYFNIGTGFATGKIDINNMIFKNTGGDTLDELTKKQOLNEI 60
DB 1 MOKNNKLSVXALPSFIDYFNIGTGFATGKIDINNMIFKNTGGDTLDELTKKQOLNEI 60
QY 61 SGKLDVNGSINDLDAQNLDTELSEIKELIKANQKRVNDVTKDAIYMLNTYLPKI 120
DB 61 SGKLDVNGSINDLDAQNLDTELSEIKELIKANQKRVNDVTKDAIYMLNTYLPKI 120
QY 121 TSWLSDVMKQNYALGQIEYLSKQKEISDKLDVINNVNLIINSTLTFPRAYQRIKYNE 180
DB 121 TSWLSDVMKQNYALGQIEYLSKQKEISDKLDVINNVNLIINSTLTFPRAYQRIKYNE 180
QY 181 KPEALTSATETNKTQDSSHDIDDELTELTELASVTKNDVGEFYANTFHDWMIGN 240
DB 181 KPEALTSATETNKTQDSSHDIDDELTELTELASVTKNDVGEFYANTFHDWMIGN 240
QY 241 NLFGRSALTYASLILAKENIKTSGSEVGNVNFILYTLALQAKAFITLTTCRKLGLADI 300
DB 241 NLFGRSALTYASLILAKENIKTSGSEVGNVNFILYTLALQAKAFITLTTCRKLGLADI 300
```

QY	301	DYTPIMNEILNKEKEEFVNILPTLSNTSNPNYEKARSGDQAKXIIMKPGYALVGE	360
Db	301	DYTPIMNEILNKEKEEFVNILPTLSNTSNPNYEKARSGDQAKXIIMKPGYALVGE	360
QY	361	ISKDSIAVLKVVQAKLKHNYOIDKDSLSIIVYGDIDKLCPDQSEOMYYTNKIAFPNEYV	420
Db	361	ISKDSIAVLKVVQAKLKHNYOIDKDSLSIIVYGDIDKLCPDQSEOMYYTNKIAFPNEYV	420
QY	421	ITKIAFTKTLNSRYEVTANFYDSSGDIIDLNKKIISSESAEFSMANNADGYMPLGT	480
Db	421	ITKIAFTKTLNSRYEVTANFYDSSGDIIDLNKKIISSESAEFSMANNADGYMPLGT	480
QY	481	SETFLTPINGFGIIVDENSRLVTLITCKSYLRETLITDLSNKEPTKLIIVPENGFSIENVEN	540
Db	481	SETFLTPINGFGIIVDENSRLVTLITCKSYLRETLITDLSNKEPTKLIIVPENGFSIENVEN	540
QY	541	GNLBEENLEPMKANNNKNAVVDHTGNGVNGTKVLYVHEDGESQITGDKLKLKTEYVLYY	600
Db	541	GNLBEENLEPMKANNNKNAVVDHTGNGVNGTKVLYVHEDGESQITGDKLKLKTEYVLYY	600
QY	601	KGKAAIYILKDEKNGDIYVEETNNLELDFQAVTKRFLITGIDS SVVHLITFSQNEEAFGN	660
Db	601	KGKAAIYILKDEKNGDIYVEETNNLELDFQAVTKRFLITGIDS SVVHLITFSQNEEAFGN	660
QY	661	FLISEIRPBEELISPELISDAMVSGQYWISGNSJNINSNVNGTFRONLSLESYSTYSM	720
Db	661	FLISEIRPBEELISPELISDAMVSGQYWISGNSJNINSNVNGTFRONLSLESYSTYSM	720
QY	721	NFNNGVFGVYTIIRNSREVVFEERSYLOFSSKYISEKFTYTTNTNGLYVELSRASSRGVINE	780
Db	721	NFNNGVFGVYTIIRNSREVVFEERSYLOFSSKYISEKFTYTTNTNGLYVELSRASSRGVINE	780
QY	781	GDPSIK 786	
Db	781	GDPSIK 786	

```

RESULT 2
US-10-452-002A-54
; Sequence 54, Application US/10452002A
; Publication No. US20030236195A1
; GENERAL INFORMATION:
; APPLICANT: Jerald S. Feltelson
; APPLICANT: H. Ernest Schnepf
; APPLICANT: Kenneth B. Narva
; APPLICANT: Brian A. Stockhoff
; APPLICANT: James L. Schweits
; APPLICANT: David Loewer
; APPLICANT: Charles J. Dullum
; APPLICANT: Judy Muller-Cohn
; APPLICANT: Lisa Stamp
; APPLICANT: George Morrill
; APPLICANT: Stacey Finnstad Lee
; TITLE OF INVENTION: No. US20030236195A1e1 Pesticidal Proteins and Methods of Using Th
; FILE REFERENCE: MA/0862D1
; CURRENT APPLICATION NUMBER: US/10/452, 002A
; PRIOR FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: 09/307,106
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 09/073,898
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 08/960,780
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: 60/029,848
; PRIOR FILING DATE: 1996-10-30
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54
; LENGTH: 787
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis strain KB59A4-6
US-10-452-002A-54

```

Query Match	5.7%	Score 45	DB 4%	Length 787
Similarity	100.0%	Pred. No. 7e-34		
Local	45	Conservative	0	Mismatches 0
Indels				Gaps 0
QY	139	EYLSKQLEISDKLDVNNNTL	INSTLTETTPAYQRIKYNEKE	183
DB	140	EYLSKQLEISDKLDVNNNTL	INSTLTETTPAYQRIKYNEKE	184

```

      RESULT 3
      US-10-698-096-25
      ; Sequence 25, Application US/10698096
      ; Publication No. US20040128716A1
      ; GENERAL INFORMATION:
      ; APPLICANT: Narva, Kenneth
      ; APPLICANT: Merlo, Donald
      ; TITLE OF INVENTION: Polynucleotides, Pesticidal Proteins, and Novel Methods of Using
      ; FILE REFERENCE: MA-708CDCl
      ; CURRENT APPLICATION NUMBER: US/10/698,096
      ; CURRENT FILING DATE: 2003-10-31
      ; PRIOR APPLICATION NUMBER: US 09/850,351
      ; PRIOR FILING DATE: 2001-05-07
      ; PRIOR APPLICATION NUMBER: US 09/073,898
      ; PRIOR FILING DATE: 1998-05-06
      ; PRIOR APPLICATION NUMBER: US 08/690,780
      ; PRIOR FILING DATE: 1997-10-30
      ; PRIOR APPLICATION NUMBER: US 60/029,848
      ; PRIOR FILING DATE: 1996-10-30
      ; NUMBER OF SEQ ID NOS: 27
      ; SOFTWARE: PatentIn version 3.1
      ; SEQ ID NO 25
      ; LENGTH: 787
      ; TYPE: PRT
      ; ORGANISM: Bacillus thuringiensis
      ; US-10-698-096-25

```

```

Query March Similarity      5.7%; Score 45; DB 4; Length 787;
Best Local Similarity     100.0%; Pred. NO. 7e-34;
Matches    45; Conservative   0; Mismatches    0; Indels    0; Gaps    0;

OY          139 EYLKQLEISDKLDVINNVNLINSTLTETTPAYORIKYVKEFE 163
|||||
|||||
|||||
Db          140 EYLKQLEISDKLDVINNVNLINSTLTETTPAYORIKYVKEFE 184
|||||
|||||
|||||

RESULT 4
US-10-698-096-27
; Sequence 27, Application US/10698096
; Publication No. US20040128716A1
; GENERAL INFORMATION:
APPLICANT: Narva, Kenneth
TITLE OF INVENTION: Polynucleotides, Pesticidal Proteins, and Novel Methods of Using
FILE REFERENCE: MA-708CDCL
CURRENT APPLICATION NUMBER: US/10/698, 096
PRIOR FILING DATE: 2003-10-31
PRIOR APPLICATION NUMBER: US 09/850,351
PRIOR FILING DATE: 2001-05-07
PRIOR APPLICATION NUMBER: US 09/073, 898
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: US 08/690, 780
PRIOR FILING DATE: 1997-10-30
PRIOR APPLICATION NUMBER: US 60/029, 848
PRIOR FILING DATE: 1996-10-30
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.1
SEQ ID NO 27
LENGTH: 788
TYPE: PRT
ORGANISM: Bacillus thuringiensis
US-10-698-096-27
```

Query Match 5.7%; Score 45; DB 4; Length 788;
Best Local Similarity 100.0%; Pred. No. 7e-34;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 139 EYLSKQKEISDKDIVINVTINLTETITPAYORITVNEKFE 183
DB 141 EYLSKQKEISDKDIVINVTINLTETITPAYORITVNEKFE 185

RESULT 5

US-10-099-285-88
; Sequence 88, Application US/10099285
; Publication No. US20030105319A1
; GENERAL INFORMATION:
; APPLICANT: Schnepf, H. Ernest
; Wicker, Carol
; Narva, Kenneth E.
; Walz, Michelle
; Stockhoff, Brian
; Muller-Cohn, Judy
; TITLE OF INVENTION: Toxins Active Against Pests
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/099,285
; FILING DATE: 15-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/002,285
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/886,615
; FILING DATE: 1-JUL-1997
; APPLICATION NUMBER: US 08/674,002
; FILING DATE: 1-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: MA-701C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 88:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 511 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 88:
US-10-099-285-88

Query Match 5.5%; Score 43; DB 4; Length 511;
Best Local Similarity 100.0%; Pred. No. 4e-32;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 KTSSEVGNVYNPLIVITLALQAKAFLLTTCRKLGLADIDYT 303
DB 122 KTSSEVGNVYNPLIVITLALQAKAFLLTTCRKLGLADIDYT 164

RESULT 6
US-10-099-285-86

; Sequence 86, Application US/10099285
; Publication No. US20030105319A1
; GENERAL INFORMATION:
; APPLICANT: Schnepf, H. Ernest
; Wicker, Carol
; Narva, Kenneth E.
; Walz, Michelle
; Stockhoff, Brian
; Muller-Cohn, Judy

; TITLE OF INVENTION: Toxins Active Against Pests
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/099,285
; FILING DATE: 15-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/002,285
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/886,615
; FILING DATE: 1-JUL-1997
; APPLICATION NUMBER: US 08/674,002
; FILING DATE: 1-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: MA-701C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 86:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 759 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 86:
US-10-099-285-86

Query Match 5.5%; Score 43; DB 4; Length 759;
Best Local Similarity 100.0%; Pred. No. 5.7e-32;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 KTSSEVGNVYNPLIVITLALQAKAFLLTTCRKLGLADIDYT 303
DB 262 KTSSEVGNVYNPLIVITLALQAKAFLLTTCRKLGLADIDYT 304

RESULT 7

US-10-698-096-19
; Sequence 19, Application US/10698096
; Publication No. US20040128716A1
; GENERAL INFORMATION:
; APPLICANT: Narva, Kenneth
; TITLE OF INVENTION: Polynucleotides, Pesticidal Proteins, and Novel Methods of Using
; FILE REFERENCE: MA-708C01
; CURRENT APPLICATION NUMBER: US/10/698,096
; PRIOR FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: US 09/850,351
; PRIOR FILING DATE: 2001-05-07

```

; PRIOR APPLICATION NUMBER: US 09/073,898
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: US 08/690,780
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 60/029,848
; PRIOR FILING DATE: 1996-10-30
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 19
; LENGTH: 786
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-698-096-19
```

```

Query Match          5.5%; Score 43; DB 4; Length 786;
Best Local Similarity 100.0%; Pred. No. 5.9e-32;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      261 KTSGEVGNVNFLLIVLTALQAKAFLLTTTCRKLGLADIDYT 303
          |||||||
Db      262 KTSGEVGNVNFLLIVLTALQAKAFLLTTTCRKLGLADIDYT 304
```

```

RESULT 8
US-10-473-687-2
; Sequence 2, Application US/10473687
; Publication No. US2004013942A1
; GENERAL INFORMATION:
; APPLICANT: Miles, Paul
; APPLICANT: Kramer, Vance
; APPLICANT: Shen, Zhicheng
; APPLICANT: Shotkoski, Frank
; TITLE OF INVENTION: Novel Pesticidal Toxins
; FILE REFERENCE: S-60000PCT
; CURRENT APPLICATION NUMBER: US/10/473,687
; CURRENT FILING DATE: 2003-09-27
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2
; LENGTH: 787
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-473-687-2
```

```

Query Match          5.5%; Score 43; DB 4; Length 787;
Best Local Similarity 100.0%; Pred. No. 5.9e-32;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      261 KTSGEVGNVNFLLIVLTALQAKAFLLTTTCRKLGLADIDYT 303
          |||||||
Db      262 KTSGEVGNVNFLLIVLTALQAKAFLLTTTCRKLGLADIDYT 304
```

```

RESULT 9
US-10-473-687-7
; Sequence 7, Application US/10473687
; Publication No. US2004013942A1
; GENERAL INFORMATION:
; APPLICANT: Miles, Paul
; APPLICANT: Kramer, Vance
; APPLICANT: Shen, Zhicheng
; APPLICANT: Shotkoski, Frank
; APPLICANT: Warren, Greg
; TITLE OF INVENTION: Novel Pesticidal Toxins
; FILE REFERENCE: S-60000PCT
; CURRENT APPLICATION NUMBER: US/10/473,687
; CURRENT FILING DATE: 2003-09-27
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 7
; LENGTH: 787
; TYPE: PRT
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```

; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(787)
; OTHER INFORMATION: Hybrid Vip3A-B Toxin
US-10-473-687-7
```

```

Query Match          5.5%; Score 43; DB 4; Length 787;
Best Local Similarity 100.0%; Pred. No. 5.9e-32;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      261 KTSGEVGNVNFLLIVLTALQAKAFLLTTTCRKLGLADIDYT 303
          |||||||
Db      262 KTSGEVGNVNFLLIVLTALQAKAFLLTTTCRKLGLADIDYT 304
```

```

RESULT 10
US-10-505-315-7
; Sequence 7, Application US/10505315
; Publication No. US20050210545A1
; GENERAL INFORMATION:
; APPLICANT: Syngenta Participations AG
; APPLICANT: Shen, Zhicheng
; APPLICANT: Warren, Gregory
; APPLICANT: Shotkoski, Frank
; APPLICANT: Kramer, Vance
; TITLE OF INVENTION: Novel Vip3 Toxins and Methods of Use
; FILE REFERENCE: 60163PCT
; CURRENT APPLICATION NUMBER: US/10/505,315
; CURRENT FILING DATE: 2004-08-19
; PRIOR APPLICATION NUMBER: US 60/362250
; PRIOR FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 7
; LENGTH: 787
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(787)
; OTHER INFORMATION: Vip3B Toxin
US-10-505-315-7
```

```

Query Match          5.5%; Score 43; DB 5; Length 787;
Best Local Similarity 100.0%; Pred. No. 5.9e-32;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      261 KTSGEVGNVNFLLIVLTALQAKAFLLTTTCRKLGLADIDYT 303
          |||||||
Db      262 KTSGEVGNVNFLLIVLTALQAKAFLLTTTCRKLGLADIDYT 304
```

```

RESULT 11
US-10-505-315-11
; Sequence 11, Application US/10505315
; Publication No. US20050210545A1
; GENERAL INFORMATION:
; APPLICANT: Syngenta Participations AG
; APPLICANT: Shen, Zhicheng
; APPLICANT: Warren, Gregory
; APPLICANT: Shotkoski, Frank
; APPLICANT: Kramer, Vance
; TITLE OF INVENTION: Novel Vip3 Toxins and Methods of Use
; FILE REFERENCE: 60163PCT
; CURRENT APPLICATION NUMBER: US/10/505,315
; CURRENT FILING DATE: 2004-08-19
; PRIOR APPLICATION NUMBER: US 60/362250
; PRIOR FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 11
; LENGTH: 788
```

TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Hybrid Vip3a-C toxin
US-10-505-315-11

Query Match 5.5%; Score 43; DB 5; Length 788;
Best Local Similarity 100.0%; Pred. No. 5.9e-32;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 KTSGSEVGNVNFIVITLALQAKAFLLTTCKRLGLADIYDT 303
DB 262 KTSGSEVGNVNFIVITLALQAKAFLLTTCKRLGLADIYDT 304

RESULT 12
US-10-505-315-32
Sequence 32, Application US/10505315
Publication No. US20050210545A1
GENERAL INFORMATION:
APPLICANT: Syngenta Participations AG
APPLICANT: Shen, Zhicheng
APPLICANT: Warren, Gregory
APPLICANT: Shokoski, Frank
APPLICANT: Kramer, Vance
TITLE OF INVENTION: Novel Vip3 Toxins and Methods of Use
FILE REFERENCE: 60163PCT
CURRENT APPLICATION NUMBER: US/10/505,315
PRIORITY FILING DATE: 2004-08-19
PRIORITY APPLICATION NUMBER: US 60/362250
PRIORITY FILING DATE: 2002-03-06
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn version 3.2
SEQ ID NO 32
LENGTH: 788
TYPE: PRT
ORGANISM: Bacillus thuringiensis
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (1)-(788)
OTHER INFORMATION: Vip3c-12168 toxin
US-10-505-315-32

Query Match 5.5%; Score 43; DB 5; Length 788;
Best Local Similarity 100.0%; Pred. No. 5.9e-32;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 KTSGSEVGNVNFIVITLALQAKAFLLTTCKRLGLADIYDT 303
DB 262 KTSGSEVGNVNFIVITLALQAKAFLLTTCKRLGLADIYDT 304

RESULT 13
US-09-850-351A-6
Sequence 6, Application US/09850351A
Patent No. US2002010080A1
GENERAL INFORMATION:
APPLICANT: Fettecson, Gerald S.
Schnepf, H. Ernest
Narva, Kenneth E.
Stockhoff, Brian A.
Schmeltz, James
Loewer, David
Dullum, Charles Joseph
Muller-Cohn, Judy
Stamp, Lisa
Morrill, George
TITLE OF INVENTION: No. US2002010080A1 Pesticidal Toxins and Nucleotide
Sequences Which Encode These Toxins
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville
STATE: FL
COUNTRY: US
ZIP: 32606-6669

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/850,351A
FILING DATE: 07-May-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/073,898
FILING DATE: 06-MAY-1998
APPLICATION NUMBER: US 08/960,780
FILING DATE: 30-OCT-1997
APPLICATION NUMBER: US 60/029,848
FILING DATE: 30-OCT-1996
ATTORNEY/AGENT INFORMATION:

NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: WA-708CD1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
TELEFAX: 352-372-5800

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 789 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: 81F

SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-850-351A-6

Query Match 5.5%; Score 43; DB 3; Length 789;
Best Local Similarity 100.0%; Pred. No. 5.9e-32;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 KTSGSEVGNVNFIVITLALQAKAFLLTTCKRLGLADIYDT 303
DB 262 KTSGSEVGNVNFIVITLALQAKAFLLTTCKRLGLADIYDT 304

RESULT 14
US-10-099-285-80
Sequence 80, Application US/10099285
Publication No. US20030105319A1
GENERAL INFORMATION:
APPLICANT: Schnepf, H. Ernest
Wicker, Carol
Narva, Kenneth E.
Walz, Michelle
Stockhoff, Brian
Muller-Cohn, Judy
TITLE OF INVENTION: Toxins Active Against Pests
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
STATE: Florida
CITY: Gainesville
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn

```

;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/099,285
; FILING DATE: 15-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/002,285
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/886,615
; FILING DATE: 1-JUL-1997
; APPLICATION NUMBER: US 08/674,002
; FILING DATE: 1-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: MA-701C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 789 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 80:
US-10-099-285-80

Query Match      5.5%; Score 43; DB 4; Length 789;
Best Local Similarity 100.0%; Pred. No. 5.9e-32;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      261 KTSGSEGVNPNFLIVLTALQAKAFLLTTCRKLGLADIDYT 303
DB      262 KTSGSEGVNPNFLIVLTALQAKAFLLTTCRKLGLADIDYT 304

RESULT 15
US-10-099-285-82
; Sequence 82, Application US/10099285
; Publication No. US20030105319A1
; GENERAL INFORMATION:
; APPLICANT: Schmeff, H. Ernest
;           Wicker, Carol
;           Narva, Kenneth E.
;           Walz, Michelle
;           Stockhoff, Brian
;           Muller-Cohn, Judy
; TITLE OF INVENTION: Toxins Active Against Pests
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentlin
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/099,285
; FILING DATE: 15-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/002,285
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/886,615
; FILING DATE: 1-JUL-1997
; APPLICATION NUMBER: US 08/674,002
; FILING DATE: 1-JUL-1996
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;
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: MA-701C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 789 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 82:
US-10-099-285-82

Query Match      5.5%; Score 43; DB 4; Length 789;
Best Local Similarity 100.0%; Pred. No. 5.9e-32;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      261 KTSGSEGVNPNFLIVLTALQAKAFLLTTCRKLGLADIDYT 303
DB      262 KTSGSEGVNPNFLIVLTALQAKAFLLTTCRKLGLADIDYT 304
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Search completed: May 15, 2006, 21:00:13
Job time : 171 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 15, 2006, 20:57:31 ; Search time 30 Seconds
(without alignments)
1230.060 Million cell updates/sec

Title: US-10-698-096-17

Perfect score: 786
Sequence: 1 MQNNKLXVALPSFIDYFN.....VELSRASSGVINFGDPSIK 786

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 250354 seqs, 46948837 residues

Total number of hits satisfying chosen parameters: 250120

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Published Applications_AA_New:*

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- 2: /SIDS5/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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- 9: /SIDS5/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 10: /SIDS5/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 11: /SIDS5/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 12: /SIDS5/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	1.0	111	9 US-10-703-799B-54	Sequence 54, Appl
2	7	0.9	64	11 US-11-087-099-12090	Sequence 12090, A
3	7	0.9	88	11 US-11-096-568A-5256	Sequence 5256, Ap
4	7	0.9	147	11 US-11-188-298-3226	Sequence 3226, Ap
5	7	0.9	152	11 US-11-264-096-2150	Sequence 2150, Ap
6	7	0.9	160	11 US-11-188-298-13227	Sequence 13227, A
7	7	0.9	174	9 US-10-873-528-124	Sequence 124, Appl
8	7	0.9	176	11 US-11-188-298-8191	Sequence 8191, Ap
9	7	0.9	199	11 US-11-096-568A-3918	Sequence 3918, Ap
10	7	0.9	206	11 US-11-232-805-69	Sequence 69, Appl
11	7	0.9	225	11 US-11-096-568A-6604	Sequence 6604, Ap
12	7	0.9	231	11 US-11-045-004-462	Sequence 462, Appl
13	7	0.9	302	11 US-11-188-298-2559	Sequence 2559, Ap
14	7	0.9	302	11 US-11-188-298-6674	Sequence 6674, Ap
15	7	0.9	316	8 US-10-196-749-54	Sequence 54, Appl
16	7	0.9	316	9 US-10-194-487-54	Sequence 54, Appl
17	7	0.9	316	9 US-10-195-883-54	Sequence 54, Appl
18	7	0.9	316	9 US-10-195-888-54	Sequence 54, Appl
19	7	0.9	316	9 US-10-195-889-54	Sequence 137, Appl
20	7	0.9	316	9 US-10-216-161A-137	Sequence 4, Appl
21	7	0.9	316	11 US-11-152-811-4	

22	7	0.9	316	11 US-11-264-096-2152	Sequence 2152, Ap
23	7	0.9	318	11 US-11-194-246-294	Sequence 294, Appl
24	7	0.9	320	11 US-11-096-568A-3789	Sequence 3789, Ap
25	7	0.9	420	11 US-11-074-176-48	Sequence 48, Appl
26	7	0.9	426	11 US-11-188-298-8092	Sequence 8092, Ap
27	7	0.9	426	11 US-11-188-298-20698	Sequence 20698, A
28	7	0.9	437	9 US-10-204-639-61	Sequence 61, Appl
29	7	0.9	458	11 US-11-232-805-46	Sequence 46, Appl
30	7	0.9	462	11 US-11-232-805-44	Sequence 44, Appl
31	7	0.9	476	11 US-11-188-298-7595	Sequence 7595, Ap
32	7	0.9	489	11 US-10-491-468-79	Sequence 79, Appl
33	7	0.9	492	9 US-10-491-468-34	Sequence 34, Appl
34	7	0.9	516	11 US-11-096-568A-27157	Sequence 27157, A
35	7	0.9	519	11 US-11-096-568A-27156	Sequence 27156, A
36	7	0.9	546	9 US-10-661-966-18	Sequence 18, Appl
37	7	0.9	563	11 US-11-087-099-4536	Sequence 4536, Ap
38	7	0.9	568	11 US-11-096-568A-27155	Sequence 27155, A
39	7	0.9	578	11 US-11-087-099-5335	Sequence 5335, Ap
40	7	0.9	599	11 US-11-188-298-15409	Sequence 15409, A
41	7	0.9	602	9 US-10-493-909-51	Sequence 51, Appl
42	7	0.9	638	11 US-11-052-554A-116	Sequence 116, Appl
43	7	0.9	643	11 US-11-087-099-5526	Sequence 5526, Ap
44	7	0.9	648	11 US-11-087-099-6188	Sequence 6188, Ap
45	7	0.9	651	11 US-11-052-554A-111	Sequence 111, Appl

ALIGNMENTS

RESULT 1
US-10-703-799B-54
Sequence 54, Application US/10703799B
Publication No. US2006007888A1
GENERAL INFORMATION:
APPLICANT: Pompeius, Markus
APPLICANT: Krogger, Burhard
APPLICANT: Schroder, Hartwig
APPLICANT: Zelder, Oskar
APPLICANT: Haberhauser, Gregor
APPLICANT: Lee, Heung-Shick
TITLE OF INVENTION: CORNEBACTERIUM GLUTAMICUM GENES ENCODING STRESS,
FILE REFERENCE: BGI-124CPN
CURRENT APPLICATION NUMBER: US/10/703,799B
CURRENT FILING DATE: 2003-11-07
PRIOR APPLICATION NUMBER: 09/603,208
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: 60/141031
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 60/142692
PRIOR FILING DATE: 1999-07-01
PRIOR APPLICATION NUMBER: 60/151214
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 19930429.7
PRIOR FILING DATE: 1999-07-01
PRIOR APPLICATION NUMBER: DE 19931413.6
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931457.8
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931541.8
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19932209.0
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932230.9
PRIOR FILING DATE: 1999-07-09
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 306
SEQ ID NO 54
LENGTH: 111
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-10-703-799B-54

Query Match 1.0%; Score 8; DB 9; Length 111;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 273 FLIVLNL 280
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Db 86 FLIVLNL 93

RESULT 2

US-11-087-099-12090
; Sequence 12090, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 12090
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(64)
; OTHER INFORMATION: unsure at all Xaa locations
US-11-087-099-12090

Query Match 0.9%; Score 7; DB 11; Length 64;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 210 ELTELAK 216
|||
Db 57 ELTELAK 63

RESULT 3

US-11-096-568A-5256
; Sequence 5256, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 5256
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(88)
; OTHER INFORMATION: Ceres Seq. ID no. 14307700
US-11-096-568A-5256

Query Match 0.9%; Score 7; DB 11; Length 88;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 349 EAKPGYA 355
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Db 12 EAKPGYA 18

RESULT 4
US-11-188-298-3226

; Sequence 3226, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 3226
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Glycine max
US-11-188-298-3226

QY 757 TTTTNT 763
|||
Db 27 TTTTNT 33

RESULT 5

US-11-264-096-2150
; Sequence 2150, Application US/11264096
; Publication No. US20060084794A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546D1
; CURRENT APPLICATION NUMBER: US/11/264,096
; CURRENT FILING DATE: 2005-11-02
; PRIOR APPLICATION NUMBER: 09/833,245
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229,358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256,931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199,384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: Patentn Ver. 2.1
; SEQ ID NO 2150
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-264-096-2150

Query Match 0.9%; Score 7; DB 11; Length 152;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 73 DLLAQN 79
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Db 89 DLLAQN 95

RESULT 6

US-11-188-298-13227
; Sequence 13227, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31

NUMBER OF SEQ ID NOS: 22569
 SEQ ID NO 13227
 LENGTH: 160
 TYPE: PRT
 ORGANISM: Oryza sativa
 US-11-188-298-13227

Query Match
 Best Local Similarity 100.0%; Score 7; DB 11; Length 160;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 382 IDKSLS 388
 Db 29 IDKSLS 35

RESULT 7
 US-10-873-528-124
 ; Sequence 124, Application US/10873528
 ; Publication No. US20050276814A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Microbial Technics Limited
 ; APPLICANT: Gilbert, Christophe FG
 ; APPLICANT: Hanebro, Philip M
 ; TITLE OF INVENTION: Proteins
 ; FILE REFERENCE: PWC/P21129MO
 ; CURRENT APPLICATION NUMBER: US/10/873,528
 ; CURRENT FILING DATE: 2004-06-23
 ; PRIOR APPLICATION NUMBER: US/09/769,787
 ; PRIOR FILING DATE: 2001-01-26
 ; PRIOR APPLICATION NUMBER: GB 9816337.1
 ; PRIOR FILING DATE: 1998-03-27
 ; PRIOR APPLICATION NUMBER: US 60/125164
 ; PRIOR FILING DATE: 1999-03-19
 ; NUMBER OF SEQ ID NOS: 388
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 124
 ; LENGTH: 174
 ; TYPE: PRT
 ; ORGANISM: Streptococcus pneumoniae
 ; US-10-873-528-124

Query Match
 Best Local Similarity 100.0%; Score 7; DB 9; Length 174;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 563 TGGVNGT 569
 Db 100 TGGVNGT 106

RESULT 8
 US-11-188-298-8191
 ; Sequence 8191, Application US/11188298
 ; Publication No. US20060075522A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Abad, Mark S. et al.
 ; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
 ; FILE REFERENCE: 38-21(53452)B
 ; CURRENT APPLICATION NUMBER: US/11/188,298
 ; CURRENT FILING DATE: 2005-07-22
 ; PRIOR APPLICATION NUMBER: 60/592,978
 ; PRIOR FILING DATE: 2004-07-31
 ; NUMBER OF SEQ ID NOS: 22569
 ; SEQ ID NO 8191
 ; LENGTH: 176
 ; TYPE: PRT
 ; ORGANISM: Glycine max
 ; FEATURES:
 ; NAME/KEY: unsure
 ; LOCATION: (1)..(176)
 ; OTHER INFORMATION: unsure at all Xaa locations
 ; US-11-188-298-8191

Query Match
 Best Local Similarity 100.0%; Score 7; DB 11; Length 176;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 98 VLVNDVT 104
 Db 72 VLVNDVT 78

RESULT 9
 US-11-096-568A-3918
 ; Sequence 3918, Application US/11096568A
 ; Publication No. US20060048240A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alexandrov, Nickolai et al.
 ; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
 ; FILE REFERENCE: 2750-1592PUS2
 ; CURRENT APPLICATION NUMBER: US/11/096,568A
 ; CURRENT FILING DATE: 2005-04-01
 ; NUMBER OF SEQ ID NOS: 34471
 ; SEQ ID NO 3918
 ; LENGTH: 199
 ; TYPE: PRT
 ; ORGANISM: Glycine max
 ; FEATURES:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)..(199)
 ; OTHER INFORMATION: Ceres Seq. ID no. 15221316
 ; US-11-096-568A-3918

Query Match
 Best Local Similarity 100.0%; Score 7; DB 11; Length 199;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 341 DKDAKIT 347
 Db 170 DKDAKIT 176

RESULT 10
 US-11-232-805-69
 ; Sequence 69, Application US/11232805
 ; Publication No. US20060073508A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Small, Kersten M.
 ; APPLICANT: Liggett, Stephen
 ; TITLE OF INVENTION: Alpha-2 Adrenergic Receptor Polymorphisms
 ; FILE REFERENCE: 10738-42D
 ; CURRENT APPLICATION NUMBER: US/11/232,805
 ; CURRENT FILING DATE: 2005-09-32
 ; NUMBER OF SEQ ID NOS: 69
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 69
 ; LENGTH: 206
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-11-232-805-69

Query Match
 Best Local Similarity 100.0%; Score 7; DB 11; Length 206;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 769 LSRASSR 775
 Db 141 LSRASSR 147

RESULT 11
 US-11-096-568A-6604
 ; Sequence 6604, Application US/11096568A
 ; Publication No. US20060048240A1

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/ GENERAL INFORMATION:
/ APPLICANT: Alexandrov, Nikolai et al.
/ TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
/ FILE REFERENCE: 2750-1592PUS2
/ CURRENT APPLICATION NUMBER: US/11/096,568A
/ NUMBER OF SEQ ID NOS: 34471
/ SEQ ID NO 6604
/ LENGTH: 225
/ TYPE: PRT
/ ORGANISM: Glycine max
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (1)..(225)
/ OTHER INFORMATION: Ceres Seq. ID no. 14315939
US-11-096-568A-6604

Query Match
Best Local Similarity 100.0%; Score 7; DB 11; Length 225;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 180 EKFELT 186
DB 176 EKFELT 182

RESULT 12
US-11-045-004-462
/ Sequence 462, Application US/11045004
/ Publication No. US20060078901A1
/ GENERAL INFORMATION:
/ APPLICANT: BUCHRIEGER, CARMEN
/ APPLICANT: FRANGEUL, LIONEL
/ APPLICANT: COUVE, ELISABETH
/ APPLICANT: RUSNIOK, CHRISTOPHE
/ APPLICANT: FSIHI, HAFIDA
/ APPLICANT: DEHOUX, PIERRE
/ APPLICANT: DUSSEURGET, OLIVIER
/ APPLICANT: CHETOUANI, FARID
/ APPLICANT: MEDJARI, HAFED
/ APPLICANT: GLASER, PHILIPPE
/ APPLICANT: KUNST, FRANK
/ APPLICANT: COSSART, PASCALE
/ APPLICANT: DANIELS, JUSTIN
/ APPLICANT: GOEBEL, WERNER
/ APPLICANT: KREFT, JURGEN
/ APPLICANT: KUHNI, MICHAEL
/ APPLICANT: NG, EVA
/ APPLICANT: VAZQUEZ-BOLAND, ANTONIO
/ APPLICANT: DOMINGUEZ-BERNAL, GUSTAVO
/ APPLICANT: GARRIDO-GARCIA, PATRICIA
/ APPLICANT: TIERREZ-MARTINEZ, ALBERTO
/ APPLICANT: AMEND, ALEXANDRA
/ APPLICANT: CHAKRABORTY, TRINAD
/ APPLICANT: DOMANN, EUGEN
/ APPLICANT: HAIN, THORSTEN
/ APPLICANT: BERGE, PATRICK
/ APPLICANT: CHARBIT, ALAIN
/ APPLICANT: DURANT, LIONEL
/ APPLICANT: PEREZ-DIAZ, JOSE-CLAUDIO
/ APPLICANT: BAQUERO, FERNANDO
/ APPLICANT: GARCIA DEL PORTILLO, FRANCISCO
/ APPLICANT: GOMEZ-LOPEZ, NURIA
/ APPLICANT: MADUENIO, ENCARNNA
/ APPLICANT: PABLOS, BETRIZ DE
/ APPLICANT: WEHLAND, JURGEN
/ APPLICANT: KARST, UWE
/ APPLICANT: ENTIAN, KARL-DIETER
/ APPLICANT: HAUF, JORG
/ APPLICANT: ROSE, MATTHIAS
/ APPLICANT: VOSS, HAMUT
/ TITLE OF INVENTION: LISTERIA MONOCYTOGENES GENOME, POLYPEPTIDES AND USES
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/ FILE REFERENCE: 05394.0018-02
/ CURRENT APPLICATION NUMBER: US/11/045,004
/ PRIOR FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: 10/637,657
/ PRIOR FILING DATE: 2003-08-11
/ PRIOR APPLICATION NUMBER: 10/257,023
/ PRIOR FILING DATE: 2002-10-08
/ PRIOR APPLICATION NUMBER: PCT/FR01/01118
/ PRIOR FILING DATE: 2001-04-11
/ PRIOR APPLICATION NUMBER: FR 00/04,629
/ PRIOR FILING DATE: 2000-04-11
/ NUMBER OF SEQ ID NOS: 2854
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 462
/ LENGTH: 291
/ TYPE: PRT
/ ORGANISM: Listeria monocytogenes
US-11-045-004-462

Query Match
Best Local Similarity 100.0%; Score 7; DB 11; Length 291;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 141 LSKOLKE 147
DB 32 LSKOLKE 38

RESULT 13
US-11-188-298-2559
/ Sequence 2559, Application US/11188298
/ Publication No. US20060075522A1
/ GENERAL INFORMATION:
/ APPLICANT: Abad, Mark S. et al.
/ TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
/ FILE REFERENCE: 38-21(53452)B
/ CURRENT APPLICATION NUMBER: US/11/188,298
/ PRIOR FILING DATE: 2005-07-22
/ PRIOR APPLICATION NUMBER: 60/592,978
/ PRIOR FILING DATE: 2004-07-31
/ NUMBER OF SEQ ID NOS: 22569
/ SEQ ID NO 2559
/ LENGTH: 302
/ TYPE: PRT
/ ORGANISM: Pseudomonas aeruginosa PA01
US-11-188-298-2559

Query Match
Best Local Similarity 100.0%; Score 7; DB 11; Length 302;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 QOLNLEI 60
DB 2 QOLNLEI 8

RESULT 14
US-11-188-298-6674
/ Sequence 6674, Application US/11188298
/ Publication No. US20060075522A1
/ GENERAL INFORMATION:
/ APPLICANT: Abad, Mark S. et al.
/ TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
/ FILE REFERENCE: 38-21(53452)B
/ CURRENT APPLICATION NUMBER: US/11/188,298
/ PRIOR FILING DATE: 2005-07-22
/ PRIOR APPLICATION NUMBER: 60/592,978
/ PRIOR FILING DATE: 2004-07-31
/ NUMBER OF SEQ ID NOS: 22569
/ SEQ ID NO 6674
/ LENGTH: 302
/ TYPE: PRT
/ ORGANISM: Pseudomonas aeruginosa UCBPP-PA14
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US-11-188-298-6674

Query Match

Best Local Similarity 0.9%; Score 7; DB 11; Length 302;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 QQLNEI 60

Db 2 QQLNEI 8

Search completed: May 15, 2006, 21:00:48
Job time : 31 secs

RESULT 15

US-10-196-749-54

; Sequence 54, Application US/10196749

; Publication No. US2006094864A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OR INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3430R1C340

; CURRENT APPLICATION NUMBER: US/10/196,749

; PRIOR FILING DATE: 2002-07-16

; PRIOR APPLICATION NUMBER: 10/052586

; PRIOR FILING DATE: 2002-01-15

; PRIOR APPLICATION NUMBER: 60/059263

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/059266

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/063120

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063121

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063486

; PRIOR FILING DATE: 1997-10-21

; PRIOR APPLICATION NUMBER: 60/063540

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063541

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063544

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 54

; LENGTH: 316

; TYPE: PRT

; ORGANISM: Homo Sapien

; FEATURE:

; NAME/KEY: unsure

; LOCATION: 233

; OTHER INFORMATION: unknown amino acid

US-10-196-749-54

Query Match

Best Local Similarity 0.9%; Score 7; DB 8; Length 316;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 73 DILAQGN 79

Db 98 DILAQGN 104

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